

F.1-10/Domain: transit peptide (amyloplast) #status predicted <TNP>  
F.71-615/Product: UDPglucose-starch glucosyltransferase #status experimental <M





```
Db 248 TLCCYACAPLILEGIIYGKCMFVNDWHSALVPVLLAAKYREYGVYRDARSVLVI 307
QY 171 HNTAFOGRMEEAFAKTKLFOAARDKLFADSGYAKVYTEATPMEDEKPLTGKTKKIN 230
Db 308 HNLAHOGVEPASTYDPLGLPPEWYGALEW-----VPEWARRHALDKG-----EAVN 354
QY 231 WLKGGIITAADKLVTSPNYATEIAADAAGGVELDTVI--RAKGIEGVINGMDIEEWNPKT 288
Db 355 FLKAVVATDRIVTVSGYSMEVTT-AGGGGCLNELLSSRSKSVLNGVINGDINDWNPST 413
QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLGVPDTPAPLEAFIGRLEPKGKGVYDIIAALPK 348
Db 414 DKFLPYHVSVDL-SGRAKCAELQKELGPIRPDVPPLIGFIGRLDYQKGDILKLAIPD 472
QY 349 ILATPKVQIALLTGKAAEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 473 LM-RDNIQFVMLSGDFEGGMRKSTESGYRDKFRGWGFSVPVSHRITAGCILLMPSR 531
QY 409 FEPGGLIQLHAMHYGTVPVVAATGGGLVDTVK-----EGVTGFHMGALNPKD 454
Db 532 FEPGGLNQLYAMQYGTVPVHGTGLRDTVENFNEFAEKGGQIGWAFSPLTIEK 586

RESULT 14
T01208
starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)
N:Alternate names: starch synthase isoform STSII-1
C:Species: Zea mays (maize)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2002
C:Accession: T01208
R:Knight, M.E.; Harn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Mu-Forester, C.;
Plant J. 14, 613-622, 1998
A:Title: Molecular cloning of starch synthase I from maize (W64A) endosperm and expressi
A:Reference number: Z14279; MUID:98340555; PMID:9675904
A:Accession: T01208
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-732 <KNT>
A:Cross-references: EMBL:AF019296; NID:g2811133; PIDN:AAD13341.1; PID:g2655029
A:Experimental source: strain W64A; endosperm
C:Genetics:
A:Gene: SSIIa
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPGlucose producing a
C:Superfamily: starch synthase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 31.5%; Score 872; DB 2; Length 732;
Best Local Similarity 39.7%; Pred. No. 5.8e-52;
Matches 211; Conservative 77; Mismatches 178; Indels 66; Gaps 15;

QY 2 LDIVMVAEVAWPWSKTGGGLGVDYTGGLPIELVKRHRVMTIAPRYDQYADAWDTSV--VVD 59
Db 241 MNVIVAAECSPWCKTGGGLGVDVGGALPALARRGHRVMTVPRYDGYEAFDGMGRKYYK 300
QY 60 IMGE--KVRYFHSIKKGVHRVWIDHPWFLAK---VWGKTGSKLYGPRSGADYLDNHRKFA 114
Db 301 AAGQDLEVNYPHAFIDGVDFVFDAPLFRHRODDIYGGSRQETM-----KRM 348
QY 115 LECKAAIEARVLP-----FGPGECCVFVANDWHSALYVLLKDEYQPKGQFTKAKSVLA 169
Db 349 LECKVAVEVPWHPVPCGGVGYDGG--NLVFIANDWHTALLPVLKAYYRDHGLMQYTRSLV 407
QY 170 IHNIAFOGRMWEAFKDTKLPOAFAFDKLFASDYAKVYTEATPMEDEKPLTGTGTYKKI 229
Db 408 IHNIAHOGRPVDEFPYMDLPHEYLQHPLELYD-----PVGG---EHA 446
QY 230 NMLKGGIITAADKLVTVSPNYATEIAADAAGGVELDTVIRAKG--IEGVINGMDIEEWNPK 287
Db 447 NIFAAGLKMADRVVTVSRGLYWELKT-VGGWGLHDIIRSDNWKINGVINGIDHGEWNEK 505
QY 288 TDKFLSAP-----YDQNSVYAGKAAKEALQAEGLGVPDTPAPLEAFIGRLEPKGKGVYDII 343
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Db 506 VDHLRSDDYTNYSLETILDAGKROCKAALRELGLLEVDRDDVPLIGFIGRLDGQKGVDIIG 565
QY 344 AALPKILATPKVQIALLTGKAAEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFM 403
Db 566 DAMFWI-AGDQVQLVMLGTGRADLERMLQHLEREPKVRGVNGVSEVPMAHRIAGADVL 624
QY 404 LVPSEFPCGLIQLHAMHYGTVPVVAATGGGLVDTVKE-----GVTFHMGALNPKDKLDEAD 459
Db 625 VMPSEFPCGLNQLYAMAYGTVPVHAVGGLRDTVAPDFPDGADLGN-----TFDRAE 678
QY 460 ADALAAIVRRASEVFA--GGRYPEMVAVNCISQDLSSWSPKPAQKWEGLLEEVVY 509
Db 679 ANKLEALRHCLDTRYKYGESWKSQARGMSQDLSWDHAAELYEDVLVAKY 730

RESULT 15
S01505
glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor - garden pea
N:Alternate names: glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor; gran
C:Species: Pisum sativum (garden pea)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Aug-2002
C:Accession: S61505; S72373; S72312
R:Dry, I.; Smith, A.; Edwards, A.; Bhattacharya, M.; Dunn, P.; Martin, C.
Plant J. 2, 193-202, 1992
A:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synt
A:Reference number: S61504; MUID:93251108; PMID:1302049
A:Accession: S61505
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-752 <DRY>
A:Cross-references: EMBL:X88790
A:Accession: S72373
A:Molecule type: protein
A:Residues: 58-59, 'H', 61-73 <DRW>
R:Edwards, E.A.
submitted to the EMBL Data Library, June 1995
A:Reference number: S72312
A:Accession: S72312
A:Molecule type: mRNA
A:Residues: 1-85, 'KVLALQRELIIQOIAERKK', 104-139, 'SSSSSAVETKRWHCQQLC', 160-752 <EDW>
A:Cross-references: EMBL:X88790; NID:g887572; PID:g887573
C:Keywords: glycosyltransferase; hexosyltransferase
F:1-57/Domain: signal sequence #status predicted <SIG>
F:58-752/Product: glycogen (starch) synthase .isoform II #status experimental <MAT>

Query Match 31.5%; Score 871; DB 2; Length 752;
Best Local Similarity 38.2%; Pred. No. 7e-52;
Matches 209; Conservative 82; Mismatches 160; Indels 96; Gaps 16;

QY 2 LDIVMVAEVAWPWSKTGGGLGVDYTGGLPIELVKRHRVMTIAPRYDQYADAWDTSV--VVD 59
Db 261 MNILYSABCAPWSKTGGGLGVDVAGSLPKALARGHRVMTIVAPHYGYAEADHIGVRRKRYK 320
QY 60 IMGE--KVRYFHSIKKGVHRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRKFA 117
Db 321 VAGQDMEVYFHYIDGVDFIDISP-----IFENLESNIY-----GSNRLDILRRMVLFC 371
QY 118 KAAIEARVLP-----FGPGECCVFVANDWHSALYVLLKDEYQPKGQFTKAKSVLAHN 172
Db 372 KAAVEVPWHPVPCGGICYGDG--NLVFIANDWHTALLPVLKAYYRDHGLMNTYRSVLVHN 430
QY 173 IAFQGRMWEAFKDTKLPOAFAFDKLFASDYAKVYTEATPMEDEKPLTGTGTYKKINWL 232
Db 431 IAHQGRG-----PVEDFNIVLSGNY.DLFKMYDPVGGEH-----FNIF 469
QY 233 KGGIIRAADKLVTVSPNYATEIAADAAGGVELDTVIRAKG--IEGVINGMDIEEWNPKTDK 290
Db 470 AAGLKATDRIVTVSHGYAWELKT-SEGWGLHNLINESDWKFRGIVNGVDTKDNWQFDA 528
QY 291 FLSP-----YDQNSVYAGKAAKEALQAEGLGVPDTPAPLEAFIGRLEPKGKGVYDIIAAL 346
Db 529 YLTSDDYTNYNLKTQTGKROCKAALQRELGLGVPREDVPITISFIGRLDHQKGVDLIAEAI 588
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run On: June 4, 2003, 13:50:41 ; Search time 7.12991 Seconds

(without alignments)

3088.950 Million cell updates/sec

Title: US-09-980-771A-9

Perfect score: 2769

Sequence: 1 ALDIVMAAEVAPWSKTGGL.....GVATAKKEIKVPAEKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1481.5	53.5	608	1	UGST_MANES
2	1457.5	52.6	607	1	UGST_SOLTU
3	1455.5	52.6	608	1	UGST_ANTMA
4	1415.5	51.1	603	1	UGST_PEA
5	1412.5	51.0	608	1	UGST_IPOBA
6	1397.5	50.5	609	1	UGST_ORYSA
7	1395.5	50.4	603	1	UGST_HORVU
8	1394.5	50.4	609	1	UGST_ORYGL
9	1362	49.2	615	1	UGST_WHEAT
10	1355.5	49.0	608	1	UGST_SORBI
11	1353.5	48.9	605	1	UGST_MAIZE
12	902.5	32.6	641	1	UGS2_SOLTU
13	873.5	31.5	626	1	UGS2_ORYSA
14	871	31.5	752	1	UGS3_PEA
15	866	31.3	610	1	UGS2_WHEAT
16	847.5	30.6	788	1	UGS3_WHEAT
17	684.5	24.7	477	1	GLGA_STREN
18	677.5	24.5	484	1	GLGA_BACSU
19	670.5	24.2	485	1	GLGA_BACST
20	669	24.2	478	1	GLGA_LACIA
21	653.5	23.6	480	1	GLG1_RHIME
22	652	23.5	480	1	GLGA_AGRU5
23	646.5	23.5	486	1	GLGA_THEMA
24	637	23.3	480	1	GLGA_RHTR
25	637	23.0	477	1	GLGA_CLOAB
26	622	22.5	482	1	GLGA_CLOPE
27	622	22.5	484	1	GLGA_VIBCH
28	614.5	22.2	476	1	GLGA_BACHD
29	604.5	21.8	486	1	GLG2_RHIME
30	604	21.8	476	1	GLGA_YERPE
31	602.5	21.8	481	1	GLGA_RHILLO
32	587	21.2	477	1	GLGA_FCOLI
33	587	21.2	477	1	GLGA_SALTI

34	580	20.9	477	1	GLGA_SALTY
35	578	20.9	480	1	GLGA_PASMU
36	569	20.5	476	1	GLGA_HAEIN
37	568.5	20.5	1230	1	UGSA_SOLTU
38	560.5	20.2	472	1	GLGA_ANASP
39	555	20.0	461	1	GLGA_FUSNN
40	552.5	20.0	463	1	GLGA_AQUAE
41	538	19.4	465	1	GLGA_SYN7
42	536	19.4	477	1	GLGA_RHOSH
43	536	19.4	492	1	GLG2_ANASP
44	535	19.3	477	1	GLGA_SYN3
45	527	19.0	444	1	GLGA_DEIRA

## ALIGNMENTS

### RESULT 1 UGST\_MANES

ID	UGST_MANES	STANDARD;	PRT;	608 AA.
AC	Q43784;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Granule-bound glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11).			
GN	WAXY OR GBSS.			
OS	Manihot esculenta (Cassava) (Manioc).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid 1; Malpighiales; Euphorbiaceae; Manihot.			
OX	NCBI_TaxID=3983;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. M.COL.22; TISSUE=Tuberous root;			
RX	MEDLINE=94083565; PubMed=8260633;			
RA	Salehuzzaman S.N., Jacobsen E., Visser R.G.F.;			
RT	"Isolation and characterization of a cDNA encoding granule-bound starch synthase in cassava (Manihot esculenta Crantz) and its antisense expression in potato."			
RT	Plant Mol. Biol. 23:947-962(1993).			
RL	CC -!- FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE STARCH.			
CC	CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) = UDP + {(1,4)-alpha-D-glucosyl}(N+1).			
CC	CC -!- PATHWAY: Starch biosynthesis.			
CC	CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.			
CC	CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS, BUT MOST ABUNDANTLY IN TUBERS.			
CC	CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE FAMILY.			

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CC	EMBL; X74160; CAA52273.1; -
DR	InterPro; IPR001296; Glycos_transf_1.
DR	Pfam; PF00534; Glycos_transf_1; 1.
KW	Glycogen biosynthesis; Transferease; Glycosyltransferase;
KW	Transit peptide; Chloroplast; Starch biosynthesis.
FT	TRANSIT 1 78 CHLOROPLAST {BY SIMILARITY}.
FT	CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT	BINDING 96 96 UDP-GLUCOSE {BY SIMILARITY}.
SQ	SEQUENCE 608 AA; 66968 MW; C9C970CD3011BDD8 CRC64;

Query Match 53.5%; Score 1481.5; DB 1; Length 608;  
Best Local Similarity 55.0%; Pred. No. 2e-92;  
Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;









DR	PIR:	S30485;
DR	PIR:	JQ2224; JQ2224.
DR	InterPro:	IPR001296; Glycos_transf_1.
DR	Pfam:	PF00534; Glycos_transf_1.
KW	Glycozen biosynthesis:	Transferase; Glycosyltransferase;
KW	Transit peptide; Chloroplast:	Starch biosynthesis.
FT	TRANSIT	1 77 CHLOROPLAST.
FT	CHAIN	78 609 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT	BINDING	97 97 UDP-GLUCOSE (BY SIMILARITY).
FT	CONFLICT	247 247 N -> T (IN REF. 5).
FT	CONFLICT	250 250 P -> T (IN REF. 5).
FT	CONFLICT	415 415 P -> S (IN REF. 4).
SQ	SEQUENCE	609 AA; 66476 MW; C225DBF6F12072C5 CRC64;

  

Query Match	50.5%;	Score 1397.5;	DB 1;	Length 609;
Best Local Similarity	51.4%;	Pred. No. 8.9e-87;		
Matches 281;	Conservative 76;	Mismatches 147;	Indels 43;	Gaps 9;

  

Qy	2	LDIWMVAEAVPWSKGTGGLGVDTGGLPTELVKRGHRVMTIAPRYDQYADAWDTSVVVDI-	60
Dd	83	MNVVFVGAEAMPSKTGSLGDLGGLPPAMAANGHVRVMISPRDYDKDAWDTSVAAEIK	142
Qy	61	--MGEKVRYEHSIKKGVHRVWIHDHPWFELAKWGCKTGSKLGPSPSGADYLDNHRFLAFC	117
Dd	143	VADRYEKRVFFHCYKRGVDVFIIDHPSLEKVGWKTEKIYGPDTGYVDYKDQMRFSLIC	202
Qy	118	KAATEAARVL-----PEGP---GEDCVFVANDWHSALVPVLLKDEYOPKGOFTKAKSVLA	169
Dd	203	QAALEAFRLNNPNFYKGTGVEDVTVVCNDWHIGPLASLYKKNYQPNGLIYNKAVAF	262
Qy	170	IHNFAOGRMWEEAFKDTKLPAQAFDKLADFSGYAKVYTEATPMEEDEXPLTGKTYKKI	229
Dd	263	IHNISYQGRFAEDYPENLNLSERPSFSDFIDGY----DTPVEG-----RKI	305
Qy	230	NWLKGGTIADKLVTSPNTATEADAAGVELDVIRAKGIEGVNGMDIEWNPXTD	289
Dd	306	NMKGAILEADRVLTVSPYYAEELISGIARGCELDNLMLRTGITGITVNGMDVSEWDPKD	365
Qy	290	KFLSAPYDONSIVAGKAAAEALQAEGLPVDTPALFAFGTLGLEOKGYDIIAALPKI	349
Dd	366	KYITAKVDATTATEAKNLKEALQAEAGLPVDRKPILFIATIGRLEEOKGPDVMAAAIPEL	425
Qy	350	LATPKVQJAITLGTKAAAYEKLVAIGNPKYKGRAGVVKFSAPLAHLMTLAGDFMLVPSRF	409
Dd	426	M-QEDVQIVLLGTGKKFEKLLKSMEKYPGKYRAVVKFNAPLAHLIMAGDVLAVPSRF	484
Qy	410	EPGLIQQLHAMHYGVTPVVAISTGGLVTVFKEGVTFGHMALNPD--KLDEADADALAATY	467
Dd	485	EPGLIQQLGMRYGTTPCACASTGGLVDTVIEGKTGFHMGRLSVDCKVVEPSDVKKVAATL	544
Qy	468	RRASEVFAGRYPEMVANCISSDLSKPAQKWEGILLEEVYVYKGG-----VATAK	518
Dd	545	KRAIKVVGPAYEEMVRNCMNQDLSRWKPAKNWNVL--LGLGVAGSAPGIEGDETAPLA	602
Qy	519	KEEIKVP 525	
Dd	603	KENVAAP 609	

  

RESULT 7	UGST_HORVU	STANDARD;	PRT;	603 AA.
ID	UGST_HORVU			
AC	P09842;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Granule-bound glycogen [starch] synthase, chloroplast precursor			
DE	(EC 2.4.1.11).			
GN	WAXY			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;			
OC	Triticeae; Hordeum.			







```

Db 300 NMWAGILEADRLVLTSPYAEELISGARGCELDNIMRLGITGIVNGMDVSEWDPRSD 359
QY 290 KFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFGRLEEQKGVDIILALPKI 349
Db 360 KYIAVKYDVSFAVEAKALNKEALQAEVGLPVDNRNIPVAFGRLEEQKGVDMVAAIPQL 419
QY 350 L-ATPKVQIATLGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPIAHMLTAGADEMLVPSR 408
Db 420 MEMVEDVOIVLGTGKKEFRMLMSAEKFPKRAVYKFNAAALAHHIMAGADVLAITSR 479
QY 409 FEPCLLIQHAMHYGTPVVAASVASTGLVDTVKEGTVGFHMGALNPD--KLDADADALAA 466
Db 480 FEPCLLIQHMRYGTPCACASTGGLVDTIIEGKTFHMGRLSDVCNVVPEADVKKVATT 539
QY 467 VRRASEVFAGRYPEMVA NCISQDLSWSKPAQKWEGLLEE--VYVGKGV-----ATAK 519
Db 540 LORAIKVVGTPAYEEMVENCMIQDLSWKGPAKNENVLLSLGVAGGEPVGEETAPLAK 599
QY 520 EEIKVP 525
Db 600 ENVAAP 605

RESULT 12
UGS2_SOLTU STANDARD; PRT; 641 AA.
AC P93568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (SS 1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Desiree; TISSUE=Leaf;
RX MEDLINE=97164391; PubMed=9011082;
RA Abel G.J.W., Springer F., Willmitzer L., Kossmann J.;
RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa
RL starch synthase from potato (Solanum tuberosum L.).";
CC Plant J. 10:981-991(1996).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Y10416; CAA71442.1; --
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 641 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 641 AA; 70608 MW; 30F8B0546CEFB74C CRC64;

Query Match 32.6%; Score 902.5; DB 1; Length 641;
Best Local Similarity 39.8%; Pred. No. 2e-53;

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Matches 212; Conservative 90; Mismatches 161; Indels 69; Gaps 19;
QY 3 DIVWAAEAPWPKTGGGLDVTGGPIELVKGHRVMTIAPRY-----DOYADAWDRS 55
Db 132 NIIFTAAAPSKTGGGDCVCSPLMAAARGHVMVSPRYLNGGSPDEKYANAVLD 191
QY 56 V--VVDIMG--EKVRYFHSIKKGVHRVWIDHPWFLAKVWKGTSKLSYGRSGADYIDNHK 111
Db 192 VRATVHCFGDAQAEVAFHEYRAGVDVFWFVDSHSSY-----RPGTP--YGDYGA--TGDNOF 244
QY 112 REALFCKAAIEARVLPFGP---GEDCVFVANDHSHALVPVLLKDEYQPKGQFTTRAKSVL 168
Db 245 RPTLLSHAACEAPLPLGFGFTYGEKCLFLANDWHAALVPLLLAAKYRPGYGVYKDAARSIV 304
QY 169 AHNIAFOGRMEWEAFKDKLPQAAFDKLAFGSDGYAKVYTEATPMEDEKPLTKTYK 228
Db 305 AHNIAHOGVEPAVTYNLGLPPQYGA---EWTFPWARAHALD-----TGET--- 351
QY 229 INWLKGIITADKLVTSVPNYATEIAADAAGVDELTVI--RAKGLEGIVNGMDEEWNPP 286
Db 352 VNVLKGALAVADRILTVSQYSWEITT--PEGYGLHLLSSRSQSVLNGITGIDVNDNP 410
QY 287 KTDKELSAFYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFGRLEEQKGVDIILAL 346
Db 411 STDEHIASHYSINDL--SGKVQCKDLQKELGPIRDCPLGIFGLRDYQKGVDIILSAI 469
QY 347 PKILATPKVQIATLGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVLP 406
Db 470 PELMQN-DVQVVMGLSGKEQYEDWNRHTENLFKDKFRAGVGVNPVSHRITAGCDILLMP 528
QY 407 SRFEPCLLIQHAMHYGTPVVAASVASTGLVDTVVK-----EGV---TGFHMGALNPDKLD 456
Db 529 SRFEPCLLIQHAMHYGTPVVAASVASTGLVDTVVKDENPYAQEGIGEGTGTWTSPLTSEKL 587
QY 457 EADADALAATVRRASEVFAGGRYP-----MVANCIQSODLSWSKPAQKWE 501
Db 588 ---LDTLKLAI-----GTYTEHKSWEGLMRGMGRDYSWENAAIQYE 627

RESULT 13
UGS2_ORYSA STANDARD; PRT; 626 AA.
AC Q40739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (SSS).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.
RC STRAIN=cv. Japonica; TISSUE=Seed;
RX MEDLINE=94302151; PubMed=7518089;
RA Baba T., Nishihara M., Mizuno K., Kawasaki T., Shimada H.,
RA Kobayashi E., Ohnishi S., Tanaka K.-I., Arai Y.,
RT "Identification, cDNA cloning, and gene expression of soluble starch
RT synthase in rice (Oryza sativa L.) immature seeds.";
RL Plant Physiol. 103:565-573(1993).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.
CC -!- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.
CC -!- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE
CC PURIFIED: RSS1, RSS2 AND RSS3.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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QY 503 LIEEVVY 509
Db 744 VIVAAKY 750

RESULT 15
UGS2 WHEAT
ID UGS2 WHEAT STANDARD; PRT; 610 AA.
AC Q43654;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycohen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. T.A. Florida; TISSUE=Endosperm;
RA Block M., Loerz H., Luetticke S.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + [(1,4)-alpha-D-glucosyl](N) =
CC UDP + [(1,4)-alpha-D-glucosyl](N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.

```

Search completed: June 4, 2003, 14:53:26  
Job time : 11.1299 secs

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```

EMBL: U48227; AB02197.1;
InterPro: IPR001296; Glycos_transf_1.
Pfam: PF00534; Glycos_transf_1; 1.
KW Glycohen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
FT NON_TER 1 1
FT TRANSIT <1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 610 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 7 7 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 610 AA; 67143 MW; 46080A3B7EB87193 CRC64;

```

Query Match 31.3%; Score 866; DB 1; Length 610;  
Best Local Similarity 39.8%; Pred. No. 5.3e-51;  
Matches 207; Conservative 78; Mismatches 161; Indels 74; Gaps 16;

```

QY 10 EVAPWSKTGGLGVDVGTGLPIELVKGHRVMTIAPRY-----DQYADAWDTISVVVDIM-- 61
Db 1 EAPYAKSGGLGVCGLSLPTALAAARGHVRVMMVRYLNGSSSDKNYAKALYAKHIKIPCF 60
QY 62 --GEKYRYPHISIKKKVHRVWIDHPFLAKVWGTGSKLYGPRSGADYLDNKHKRFALFCKA 119
Db 61 GGSHEVTEFFHEYRDNDVDFVDHP-----SYHRPGS-LYGDNFGA-FGDNQFRITLLCYA 113
QY 120 ATEAARVLFGP---GEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLAHNIAFQ 176
Db 114 ACEAPLILLEGGYIYGQNCMFVNDWHSALVPVLLAAKVPYGVYRDSRSTLVHNLAHQ 173
QY 177 GRMWEAEAKDTLPQAAFDKLAFLSDGAKYVTEATFWEDEKPLTGKTKYNLWLGKI 236
Db 174 GVEPASTYDGLGLPPWYGALW-----VFPEWARRHLDKG-----EAVNFLKGAV 220
QY 237 IAADKLVTSPNYATEIAADAAGGVELDTVI--RAKIGIEIYNGMDIEEWNPKTKDFLSA 294

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Db 221 VTADRIVTYSQGYSEVIT-ABGGQGLNELLSSKSVLNGIVNGIDINDWNPTDKCLPH 279
QY 295 PYDQNSVYAGKAAKEALQALGLPVDPTAPLFAFGRLEEQKGVDIILAAALPKILATPK 354
Db 280 HYSVDDL-SGKAKCAELQKELGLPVREDVPLIGFTIGRLDYOKGIDLIKMAIPELM-RED 337
QY 355 VOAILGTGKAAYEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADEMLVPSRPPCGL 414
Db 338 VQFVMLGSGDPIFEGWMSRSTESSYKDKFGWVGFVPSVSHRTAGCDIILMPSRPPCGL 397
QY 415 IQLHAMHYGTVPVAVASTGGGLVDTVK-----EGVTGFHMGALNPDKIDADADALAA 465
Db 398 NOLYAMQYGTVPVWHGTGGLRDTVETNPFNFGAKGEEGTGWAFSPLTVDKMLWA----- 450
QY 466 TVRRASEVFAAGRYPEMWANCISQDLSWSKPAQKWEGLLE 505
Db 451 -LRTAMSTFRE-----HKPS--WEGLMK 470

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:35:26 ; Search time 26.3807 Seconds  
(without alignments)  
4147.394 Million cell updates/sec

Title: US-09-980-771A-9  
Perfect score: 2769  
Sequence: 1 ALDIVMAAEVAPNSKTGGL.....GGVATAKKEIKVPVAKIP 531

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phase:.\*  
10: sp\_plant:.\*  
11: sp\_rodent:.\*  
12: sp\_virus:.\*  
13: sp Vertebrate:.\*  
14: sp Unclassified:.\*  
15: sp\_rvirus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2765	99.9	708	10	064925
2	1463.5	52.9	613	10	Q93YB1
3	1450.5	52.4	604	10	Q9FR03
4	1424.5	51.4	608	10	Q93VD9
5	1423.5	51.4	606	10	Q9XIS6
6	1423.5	51.4	607	10	Q9XSQ5
7	1404	50.7	608	10	Q8VYU1
8	1397.5	50.5	609	10	Q94LY7
9	1395.5	50.4	603	10	Q8SA49
10	1390	50.2	610	10	Q9WAQ0
11	1389.5	50.2	609	10	Q8S9C4
12	1381	49.9	605	10	Q9SXX3
13	1380	49.8	605	10	Q9FU06
14	1379	49.8	599	10	Q9SQ58
15	1376	49.7	606	10	Q43012
16	1375	49.7	604	10	Q9S7N5
					Q9S7N5 triticum ae

17	1371	49.5	534	10	Q8W2G8
18	1369	49.4	604	10	Q9SLS6
19	1367.5	49.4	604	10	Q9SLS7
20	1367	49.4	605	10	Q9SQ51
21	1366	49.3	605	10	Q9SLS8
22	1362.5	49.2	604	10	Q9SXX4
23	1360.5	49.1	604	10	Q9SLS9
24	1354.5	48.9	605	10	Q9SQ52
25	1353.5	48.9	574	10	Q9SYU0
26	1263.5	45.6	565	10	Q9XEN9
27	898	32.4	792	10	Q9MAC8
28	895.5	32.3	313	10	Q9LKD3
29	893.5	32.3	313	10	Q9LKE0
30	893.5	32.3	313	10	Q9FYU8
31	891.5	32.2	647	10	Q9LEB9
32	891.5	32.2	647	10	Q9SQH0
33	891.5	32.2	647	10	Q9SQG9
34	890.5	32.2	647	10	Q9LECO
35	886.5	32.0	313	10	Q9LKE8
36	886	32.0	576	10	064926
37	885.5	32.0	313	10	Q9LKD1
38	884.5	31.9	643	10	Q9M5A3
39	879.5	31.8	313	10	Q9LKE5
40	879.5	31.8	313	10	Q9LKD6
41	878.5	31.7	313	10	Q9LKE7
42	878.5	31.7	313	10	Q9LKE1
43	877.5	31.7	313	10	Q9LKE6
44	877.5	31.7	313	10	Q9LKD8
45	876.5	31.7	313	10	Q9LKE5

## ALIGNMENTS

## RESULT 1

064925 PRELIMINARY; PRI: 708 AA.  
AC 064925;  
DT 01-AUG-1998 (TREMREL. 07, Created)  
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).  
GN STA2.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=137C;  
RA D'Hulst C., Wattlebled F., Ral J.-P., Abel G.J., Kossmann J.,  
RA Ball S.G.;  
RT "Cloning of a cDNA encoding for the GBSSI in the green alga  
Chlamydomonas reinhardtii.";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Wattlebled F., Ball S.G., D'Hulst C.;  
RT "Granule-bound starch synthase I: A major enzyme involved in the  
biogenesis of B-crystallites in starch granules.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026420; AAC1969.3;  
DR EMBL; AF43156; AAL28128.1;  
DR InterPro; IPR001296; Glycos\_transf\_1.  
DR InterPro; IPR002114; HPI\_SerP\_site.  
DR Pfam; PF00534; Glycos\_transf\_1;  
DR PROSITE; PS00589; PTS\_HPR\_SER; UNKNOWN\_1.  
DR Glycosyltransferase; Transferase; Trans peptide.  
FT TRANSIT 1 57 POTENTIAL  
FT CHAIN 58 708 GRANULE-BOUND STARCH SYNTHASE I.  
SQ SEQUENCE 708 AA; 74623 MW; 7D2A5A07D8606469 CRC64;

Query Match

99.9% Score 2765; DB 10; Length 708;

[illegible]

```

RESULT 2
Q93YBI PRELIMINARY; PRT; 613 AA.
ID Q93YBI;
AC Q93YBI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.11).
GN GBSSI.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Edwards A., Vincken J.P., Visser R., Zeeman S., Smith A.M., Martin C.;
RT "Discrete Forms of amylose are synthesised by isoforms of GBSSI in
RT pea."
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ345045; CAC69955.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR001917; NHTransf_2.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
DR Glycosyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 85
FT CHAIN 86 613 GRANULE BOUND STARCH SYNTHASE.
FT SEQUENCE 613 AA; 67626 MW; 5A653461128F97EB CRC64;
Query Match 52.9%; Score 1463.5; DB 10; Length 613;
Best Local Similarity 53.0%; Pred No. 1.1e-91;

```

[illegible]



Query Match 51.4%; Score 1423.5; DB 10; Length 606;  
 Best Local Similarity 51.5%; Pred. No. 5.8e-89;  
 Matches 282; Conservative 82; Mismatches 139; Indels 45; Gaps 10;

QY 2 LDIYVAAEAPVAPSKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDIM 61  
 DB 80 MNLFVGAEAPVAPSKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDIM 139  
 QY 62 G----EKVRYFHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKHKRFALFC 117  
 DB 140 VADRIETVRFHCHYKQGVDRVFDHPCFLEKVGKTSKLYGPRSGADYLDNKHKRFALFC 199  
 QY 118 KAALAEARVLPF-----GP-GEDCVFVANDHSAVLPVLLKDEYQPKGQFTKAKSVLA 169  
 DB 200 QAALAEARVLPF-----GP-GEDCVFVANDHSAVLPVLLKDEYQPKGQFTKAKSVLA 259  
 QY 170 IHNIAFOGRMWEAFKDKLP---QAADFKLAFSDGYAKVYTEATPMEDEKPPLTGKTY 226  
 DB 260 IHNISYQGRPFEDFLLNLPNEYRSADF--FDGHLK-----PVRG--- 299  
 QY 227 KKNLWKGIIAADKLVTVSPNYATEATAAAGGVVELDTVIRAKGIEGIVNGMDIEEWN 286  
 DB 300 KKNWKAALLESDLTVTSPIYAKELVSGEDRGVLDNIIKRTGVAGIVNGMDIREWSP 359  
 QY 287 KTDKFLSAPYDONSIVYAGKAAKALQAEGLPVDPTAPLFAFTGRLEOKGVDIIILAL 346  
 DB 360 KTDKFLSAPYDONSIVYAGKAAKALQAEGLPVDPTAPLFAFTGRLEOKGVDIIILAL 419  
 QY 347 PKILATPKVQITAILGTGKAAYEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVLP 406  
 DB 420 PKFI-DONVOIILGTGKSWEQIELEIPEKARGIAKFDGFLAHKIAGSDFMIP 478  
 QY 407 SRPEPCGLIOLHAMHYGTVPVASTGGTGLVDTVKEGVTGFHMGALNP--KLDEADADALA 464  
 DB 479 SRPEPCGLVQHSMPYGTVPVASTGGTGLVDTVKEGVTGFHMGALNP--KLDEADADALA 538  
 QY 465 ATVRASEVPAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYGG-----GVATA 517  
 DB 539 TTVRRALGTGTVAMEKIIQNCMAQDFSWKPAQKWEGLLEEVYVYGG-----GVATA 598  
 QY 518 KKEEIKVP 525  
 DB 599 AKENVATP 606

RESULT 6  
 Q9ZSQ5 ID Q9ZSQ5 PRELIMINARY; PRT; 607 AA.  
 AC Q9ZSQ5;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAR-2002 (Tremblrel. 10, Last sequence update)  
 DE Granule-bound glycogen (starch) synthase (EC 2.4.1.11).  
 OS Astragalus membranaceus (Milk vetch) (Huang qi).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Galegeae; Astragalus.  
 OX NCBI\_TaxID=83837;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-HAIRY ROOTS INDUCED BY RHIZOGENESIS AGROBACTERIUM LBA9402;  
 RA Peng J.S., Liu D., Hu Z.B.;  
 RT "cDNA cloning and structural analysis of granule-bound starch synthase  
 RT gene of Astragalus membranaceus";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF097922; AC70779.1;  
 DR InterPro; IPR001296; Glycos\_transf\_1.  
 DR Pfam; PF00534; Glycos\_transf\_1; 1.  
 KW Glycosyltransferase; transferase.  
 SQ SEQUENCE 607 AA; 66560 MW; 61BB0CACB94D387C CRC64;

Query Match 51.4%; Score 1423.5; DB 10; Length 607;  
 Best Local Similarity 52.7%; Pred. No. 5.8e-89;

Matches 289; Conservative 74; Mismatches 140; Indels 45; Gaps 12;

QY 2 LDIYVAAEAPVAPSKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDI- 60  
 DB 81 MNLFVGAEAPVAPSKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDI 140  
 QY 61 MG----EKVRYFHSIKKGVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKHKRFALFC 117  
 DB 141 VADRIETVRFHCHYKQGVDRVFDHPCFLEKVGKTSKLYGPRSGADYLDNKHKRFALFC 200  
 QY 118 KAALAEARVLPF-----GP-GEDCVFVANDHSAVLPVLLKDEYQPKGQFTKAKSVLA 169  
 DB 201 QAALAEARVLPF-----GP-GEDCVFVANDHSAVLPVLLKDEYQPKGQFTKAKSVLA 260  
 QY 170 IHNIAFOGRMWEAFKDKLP---TKLPQAAFDKLAFSDGYAKVYTEATPMEDEKPPLTGKTY 226  
 DB 261 IHNIAFOGRMWEAFKDKLP---TKLPQAAFDKLAFSDGYAKVYTEATPMEDEKPPLTGKTY 300  
 QY 227 KKNLWKGIIAADKLVTVSPNYATEATAAAGGVVELDTVIRAKGIEGIVNGMDIEEWN 286  
 DB 301 KKNWKAALLESDLTVTSPIYAKELVSGEDRGVLDNIIKRTGVAGIVNGMDIREWSP 360  
 QY 287 KTDKFLSAPYDONSIVYAGKAAKALQAEGLPVDPTAPLFAFTGRLEOKGVDIIILAL 346  
 DB 361 KTDKFLSAPYDONSIVYAGKAAKALQAEGLPVDPTAPLFAFTGRLEOKGVDIIILAL 420  
 QY 347 PKILATPKVQITAILGTGKAAYEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVLP 406  
 DB 421 PKFI-DONVOIILGTGKSWEQIELEIPEKARGIAKFDGFLAHKIAGSDFMIP 479  
 QY 407 SRPEPCGLIOLHAMHYGTVPVASTGGTGLVDTVKEGVTGFHMGALNP--KLDEADADALA 464  
 DB 480 SRPEPCGLVQHSMPYGTVPVASTGGTGLVDTVKEGVTGFHMGALNP--KLDEADADALA 539  
 QY 465 ATVRASEVPAGGRYPPEMVANCISODLSWSKPAQKWEGLLEEVYVYGG-----GVATA 517  
 DB 540 TTVRRALGTGTVAMEKIIQNCMAQDFSWKPAQKWEGLLEEVYVYGG-----GVATA 599  
 QY 518 KKEEIKVP 525  
 DB 600 AKENVATP 607

RESULT 7  
 Q8VYU1 ID Q8VYU1 PRELIMINARY; PRT; 608 AA.  
 AC Q8VYU1;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DE Granule binding starch synthase II.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eubartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wu P., Duan W.M., Jiang H.W.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY069940; AAL58572.1;  
 DR InterPro; IPR001296; Glycos\_transf\_1.  
 DR Pfam; PF00534; Glycos\_transf\_1; 1.  
 SQ SEQUENCE 608 AA; 67327 MW; D960662542E9400E CRC64;

Query Match 50.7%; Score 1404; DB 10; Length 608;  
 Best Local Similarity 51.5%; Pred. No. 1.3e-87;  
 Matches 283; Conservative 72; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIYVAAEAPVAPSKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDI- 60  
 DB 81 MTLIFATECHPWCKTGGTGLGDTGGTGLPIELVKRGHVMVTIAPRYDQYADAWDTSVVVDI 140

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QY 61 ---MGEKVRFFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRFALFC 117
Db 141 IGDRIETVFFHCYKKGVDVRFVDHPFLEKVGWKTGPKLYGTTGDDYRDNQRLFCCLLC 200
QY 118 KAAIEARVLPF-----GP-GEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLA 169
Db 201 LAALAPRVLNLNNSSEYFSGPYGENVVFVANDWHTGVLPCYLKSIQAQGMVNAKVAFC 260
QY 170 IHNIAFOGRMWEAFKDTKLPOAADFKLAFSDCYAKVYTEATPMEDEKPLTGKTYKKI 229
Db 261 IHNIAVQGRFAREDPELLNPDSPFLPSFDFIDGHEK-----PVG-----RKI 303
QY 230 NWLKGIIAADKLVTSPNYATEIAADAAGGVLELTVIRAKGIE-GIVNGMDIEEWNPKT 288
Db 304 NWKAGITCEDLMVSPHYVELASGPKGVLELGLITKPLETGIVNGMDVIEYENPAT 363
QY 289 DKFELSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFAGRLFEQKGVDTIIAALPK 348
Db 364 DQYISVKYDATVTEARALNKEMQLQAEVGLPVDSSILPIVFGRLSEQKSDILIAAIE 423
QY 349 ILATPKVOIALIGTGKAAEYKLVNAIGTKYKRAKGVVKTSPAPLAHMLTAGADEMLVPSR 408
Db 424 FV-EGNVQLIVLGTGKKKMEELILLEVKYPTARGLAKFNYPPLAHMFPAGADFIIVPSR 482
QY 409 FEPGGLIQLHAMHYGTVPVVASTGGLVDTVKEGTVGFHMGALNP--DKLDEADADALAT 466
Db 483 FEPGGLIQLQGMRYGVVPCSTGGLVDTVKEGTVGFHMGALNPVCETVDPVDVAVAST 542
QY 467 VRASEVFAGRYPPEMVANCSODLSWSKPAQKWEGLLEEVYVYKGG-----GVA 515
Db 543 VKRALQYNTAFQEMQVNCMAQDLSWKGPAKKV---EEVLGLGVGESSQPIGSEVA 598
QY 516 TAKKEIKVP 525
Db 599 PLAKENVATP 608

```

## RESULT 8

```

Q94LY7
ID Q94LY7 PRELIMINARY; PRT; 609 AA.
AC Q94LY7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.21).
GN WAXY
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. REMONT;
RA Larkin P.D., McClung A.M., Ayres N.M., Park W.D.;
RT "The Wx locus (Granule Bound Starch Synthase) is strongly associated
RT with pasting curve characteristics in rice (Oryza sativa L.).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141954; AAF72561.1;
DR InterPro; IPR001296; Glycos_transf.1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf.1.1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
SQ SEQUENCE 609 AA; 66466 MW; 6D2615EB203CBDC8 CRC64;

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Query Match 50.5%; Score 1397.5; DB 10; Length 609;
Best Local Similarity 51.4%; Pred. No. 3.5e-87;
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;
QY 2 LDIWVAAEAVAPWSKTKGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKTKGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI- 142

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QY 61 ---MGEKVRFFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRFALFC 117
Db 143 VADRYERVRFHCYKRGVDVRFIDHPFLEKVGWKTGKLYGPDYDVKDNQMRSLC 202
QY 118 KAAIEARVLPF-----PFGP---GEDCVFVANDWHSALVPVLLKDEYQPKQFTKAKSVLA 169
Db 203 QAALEAPRILNLNNSNPFYKTYGIDYVFCNDWHTGPLASLYKNNTYQNGIYRNAKVAFC 262
QY 170 IHNIAFOGRMWEAFKDTKLPOAADFKLAFSDCYAKVYTEATPMEDEKPLTGKTYKKI 229
Db 263 IHNISVQGRFAFEDYDELNLSEPRSRFIDIGY-----DTFVEG-----RKI 305
QY 230 NWLKGIIAADKLVTSPNYATEIAADAAGGVLELTVIRAKGIEGIVNGMDIEEWNPKTD 289
Db 306 NWKAGILEADRVLTSPVYAEELISGIARGCELDNIMRLTGTGIVNGMDVSEWPSKD 365
QY 290 KFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFAGRLFEQKGVDTIIAALPKI 349
Db 366 KYITAKYDATTATEAKALNKALQAEGLPVDPRKIPLIATFAGRLFEQKGVDTIIAALPKI 425
QY 350 LATPKVOIALIGTGKAAEYKLVNAIGTKYKRAKGVVKTSPAPLAHMLTAGADEMLVPSR 409
Db 426 M-QEDVQIVLLGIGKKKPEKLLKSMEEKYKGVKRAVVKFNAPLAHMLTAGADVLVPSR 484
QY 410 EPGGLIQLHAMHYGTVPVVASTGGLVDTVKEGTVGFHMGALNP--KLDEADADALATV 467
Db 485 EPGGLIQLQGMRYGTPCACASTGGLVDTVIEGTFGHMGRSLVDCKVVFSDVKKVAATL 544
QY 468 RRASEVFAGRYPPEMVANCSODLSWSKPAQKWEGLLEEVYVYKGG-----VATAK 518
Db 545 KRAIKVGPVPAYEEMVRNCMQDLSWKGPAKKWENVL--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEEIKVP 525
Db 603 KENVAAP 609

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## RESULT 9

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Q8SA49
ID Q8SA49 PRELIMINARY; PRT; 603 AA.
AC Q8SA49;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Granule-bound starch synthase.
GN 259116.5.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MEREK;
RA Ma J., Sanmiguel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
RA Jiang Z., Bussio C.S., Kleinhofs A., Devos K.M., Ramakrishna W.,
RA Bennetzen J.L.;
RT "Comparative sequence analysis of Wx1 homologous regions in barley,
RT maize, pearl millet, rice, sorghum and diploid wheat.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF474373; AAL77109.1;
SQ SEQUENCE 603 AA; 66280 MW; 467A3DE6A82125CB CRC64;

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Query Match 50.4%; Score 1395.5; DB 10; Length 603;
Best Local Similarity 53.3%; Pred. No. 4.7e-87;
Matches 277; Conservative 71; Mismatches 141; Indels 31; Gaps 7;
QY 2 LDIWVAAEAVAPWSKTKGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI 61
Db 76 MNVVFVGAEMAPWSKTKGLGVDVGTGGLPIELVKRHRVMTIAPRYDQYADAMDTSVVVDI 135
QY 62 ---GEKVRFFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRFALFC 117

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136	VADEYERVRFFHCYKRGVDVRFIDHPWFLBKVRGKTEKGIYGPAGTDYEDNQOBFSLIC	199
118	KAAIEAARVL-----PF--GP-GECDYFVANDWHSALVPVLLKDEYQPKGOTFAKSVALA	169
196	QAALEAPRILNNNNPYFSGPYGEDVYFVNCNDWHTGLLACVLYKSNYQSNGIYRTAKVAFVC	255
170	IHNIAFCGRMWEEAFKDTKLPQAAFDKLAISDGYAKVYTEAIPMEEDEKPELTGYKTYEKI	229
256	IHNISYQGRFSFDDFAQLNLPDRFKSSFDIDGYDK-----PVEG---RKI	298
230	NWLKGGIIAADKLVTSPNATETAADAAGGVELDTVIRAKGIEGIVNMDIEEWNPKTD	289
299	NWMAKQLQADKVLVTSPYYABEELISGEARGCELDNMLRTGITGIVNMGDVSEWDPKFD	358
290	KFLSAPYDQNSYVAGKAAAEALQAEGLPLVDPTAPLFAFICRLEEQRGVDIILAALPKI	349
359	KFLAVNYDITTALEAKKALNKEALQAEVGLPVDRKVPVFAFICRLEEQRGVDMIAAIEPI	418
350	LATPKVQIAILGTGKAAEYKLVNAIGIKYKCRAGVYKFSAPLAHMLTAGADFMLVPSRF	409
419	LKPEDVQIILGTGKKKFEKLLKSMEEKFPQKVRVVRFNAPLAHOMMAGADLLAVTSRF	478
410	EPGLLIQLHAMHYGTPVWASTGGLVDTVKGVTFGHMGALNPD--KLDEADADALAATV	467
479	EPGLLIQLQMRNYGTPCVCASTGGLVDTIVGSKTGFHMGRLSVDNCNVVEPADVKKVAITL	538
468	RRASEYFAGGRYPENWANCISQDLSWSKPAQKWEGILLEEV	507
539	KRAVKVYGTIPAYQBMVKNCMIQDLSWKGPAPKNWEDVLEEL	578

## RESULT 10

Q9MAQ0 PRELIMINARY; PRT; 610 AA.

AC	Q9MAQ0:	
AD	01-OCT-2000 (TrEMBLrel. 15, Created)	
AE	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
AF	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
AG	granule-bound starch synthase.	
AH	R9L11.8.	
AI	Arabidopsis thaliana (Mouse-ear cress).	
AJ	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AK	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
AL	OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.	
AM	OC NCBI_taxid=3702;	
AN	[1]	
AO	SEQUENCE FROM N.A.	
AP	STRAIN=CV. COLUMBIA;	
AQ	RC Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,	
AR	RA Altafi H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin C.,	
AS	RA Chioiu J., Choi E., Dunn P., Gonzalez A., Hong B., Kim C., Koo T.,	
AT	RA Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,	
AV	RA Pham P., Sakano H., Schwartz J., Shinn P., Thaveris A., Toriumi M.,	
AW	RA Vaysberg M., Walker M., Yu G., Eckel J., Theologis A., Davis R.W.,	
AX	RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.	
AY	RL EMBL; AC006424; AAF31273.1;	
AZ	DR InterPro: IPR001296; Glycos.transf.1.	
BA	DR Pfam: PF00534; Glycos.transf.1.	
BB	DR SEQUENCE 610 AA: 66879 MW: 6817F25BE12220DF CRC64;	
BC	SD	

204	QAALEAPQVNLNSSKVFSGPYGEDVVFVANDHHTALLPCYLKSMYQSRGVYNNAKVVC	263
170	IHNIAFGQRMWEAFKDKLP---QAADFCLAFSDGYAKVYTEATPMEDEKPLTKTY	226
264	IHNIAFGQRFADYSLNLNPISEKSSFD---FMDGYEK-----PVKG---	303
227	KKINWLKGGIIAADKLVTSNPYATEIAADAAGGVELDTVIRAKTEGIVNGMDIEWNP	286
304	RKINMKAAILEAHRVLTVSPYIAQELISGWDRGVELHKLRMKTVTSINGMDVQWNP	363
287	KTDKFISAPYDQNSVYAGKAAAEALQALGLPDPAPLFAFAGRLEEKGVDIILAAL	346
364	STDYIDIDKYDITVTDAKPLIKEALQAAYGLPVRDPVPVIGFIRGLEEKGSDILVEAI	423
347	PKLIATPKVOIALTGKAAAYELVNNAIGTKYKGRAGGVVKFSAPLAHMLTAGADFLVP	406
424	SKTMGL-NVQMVLILGTGKKKMEAOILEEKEFKPGKAVGVAKFNVP LAHMLTAGADFLVP	482
407	SRFEPCCGLIQIHAMHYGTVPVASTGGLGVDTVKEGVTGFHMGALNP--DKLDEADADALA	464
483	SRFEPCCGLIQIHAMRYGTVPVASTGGLGVDTVKDYTGFGFHGRFNVKCEVVDPDPVIATA	542
465	ATVRRASEVFAGGYPENWANCISQDIJSWKSFAQKWEGLLLEVVYVGGGVATAKKEIKV	524
543	KAVTRAVAYGTSAMQEMWKNMCDQDFSWKGFAELWEKVLISLNLVA-GSEAGTEGEET-A	600
525	PVAEK 529	
601	PLAKE 605	

RESULT 11

Q8S9C4

ID Q8S9C4 PRELIMINARY; PRT; 609 AA.

AC Q8S9C4;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Starch granule-bound starch synthase.

GN wx-1.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.

OC NCBI\_TaxID=4530;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=CV. MILKY QUEEN;

RC Sato H., Suzuki Y., Sakai M., Imbe T.;

RA "Molecular Characterization of wx-1, a Novel Mutant Gene for Low-

RT amylose Content in Endosperm of Rice (*Oryza sativa* L.).";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RR EMBL; AB06093; BAB88209.1; -

RQ SEQUENCE 609 AA; 66431 MW; B57CC13E0440D227 CRC64;

Query Match 50.2%; Score 1389.5; DB 10; Length 609;

Best Local Similarity 51.2%; Pred. NO. 1.2e-86;

Matches 280; Conservative 76; Mismatches 148; Indels 43; Gaps 9;



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Db 263 IHNISYQGRKFAFEDYPELNSERFRSSDF IDGY-----DTPVEG-----RKI 305
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWNPMTD 289
Db 306 NMWAGILEADRVLTSPYIAEELISGTARGCELDNIMRLTGTITGIVNGMDVSEWDPKSD 365
QY 290 KFLSAPYDONSUYAGKAAKEALQAEGLPLVDPTAPLFAFIRLEEQKGVDTIILALPKI 349
Db 366 KYITAKYDATTAEIAKALNKALQAEGLPDRKIPLFAFIRLEEQKGVDMMAAIPEL 425
QY 350 LATPKVQIAILGTGKAAEYKLVNAITGTYKGRAGKGVKFSAPLAHMLTAGADMVLPSPRF 409
Db 426 M-QEDVQVLLGTGKKEKELLSMEKYPGKVRVAVKFNAPLAHMLTAGADMVLPSPRF 484
QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDTVKGVTFHMGALNPD--KLDEADADALAATV 467
Db 485 EPCGLIQLQGMRYGTTPCACASTGGGLVDTVIEGKTGFHMGRLSVDCVKVEPSDVKKVAATL 544
QY 468 RRASEVFAGGRYPPEMVANCISODLSWSKPAOKWEGLEEYVYKGG-----VATAK 518
Db 545 KRAIKVVGTPAYEEMVRNQMQLSWKGPARNWNLV--LGLGVAGSAPGIEGDEIAPLA 602
QY 519 KEEIKVP 525
Db 603 KENVAAP 609

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## RESULT 12

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Q9SXX3 ID Q9SXX3 PRELIMINARY; PRT; 605 AA.
AC Q9SXX3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Starch synthase (GBSSI) (EC 2.4.1.21).
GN WAXY.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99321800; PubMed=10393240;
RX Murai J., Taira T., Ohta D.;
RT "Isolation and characterization of the three waxy genes encoding the
RT granule-bound starch synthase in hexaploid wheat.";
RL Gene 234:71-79(1999).
DR EMBL; AB019623; BAA77351.1; -.
DR InterPro; IPR001296; Glycosyl-transf_1.
DR Pfam; PF00534; Glycosyl-transf_1.
DR PROSITE; PS00606; B_KETOACYL-SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66345 MW; 60A816276F78722B CRC64;

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Query Match 49.9%; Score 1381; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 4.6e-86;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
QY 2 LDIVMAAEVAPWSKTTGGLGVDTGGLPIELVKRGRHVTMTAPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFCVCAEAPWSKTTGGLGVDTGGLPPMAANGHRVMTISPRYDQYKDAWDTSVVSEIK 137
QY 62 ----GEKRVYFHSIKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKHRRALFC 117
Db 138 VADEYERVRVHCYKRGVDRVFDHPCFLKVRGKTKYKIGPDAGTDYEDNQLRFSLLC 197
QY 118 KAAIEARVL-----PF--GP-GEDEVFVANDHMSALVPVLLKDEYQPKQFTKAKSVLA 169
Db 198 QAALEAPRILDDNNNPFSGPYGDEVVVCNWDHNTGLLACYLKSNGYSSGIYRTAKVAF 257

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QY 170 IHNIAFQGRMBEAFKDTKLPOAAFDFKLAESDGIYAKVYTEATPMEDEKEPPLTGKTYKI 229
Db 258 IHNISYQGRFSDFDFAQLNLPDRFKSSDF IDGYDK-----PVEG-----RKI 300
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWNPMTD 289
Db 301 NMWAGILEADRVLTSPYIAEELISGTARGCELDNIMRLTGTITGIVNGMDVSEWDPKSD 360
QY 290 KFLSAPYDONSUYAGKAAKEALQAEGLPLVDPTAPLFAFIRLEEQKGVDTIILALPKI 349
Db 361 KYITAKYDATTAEIAKALNKALQAEGLPDRKIPLFAFIRLEEQKGVDMMAAIPEL 420
QY 350 LATPKVQIAILGTGKAAEYKLVNAITGTYKGRAGKGVKFSAPLAHMLTAGADMVLPSPRF 409
Db 421 LKEEDVQVLLGTGKKEKELLSMEKYPGKVRVAVKFNAPLAHMLTAGADMVLPSPRF 480
QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDTVKGVTFHMGALNPD--KLDEADADALAATV 467
Db 481 EPCGLIQLQGMRYGTTPCACASTGGGLVDTVIEGKTGFHMGRLSVDCNVVEPADVKKVVTTL 540
QY 468 RRASEVFAGGRYPPEMVANCISODLSWSKPAOKWEGLEEYVYKGGVATAK 519
Db 541 KRAIKVVGTPAYEEMVRNQMQLSWKGPARNWNLV--LGLGVAGSAPGIEGDEIAPLA 599
QY 520 KEEIKVP 525
Db 600 KENVAAP 605

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## RESULT 13

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Q9FUU6 ID Q9FUU6 PRELIMINARY; PRT; 605 AA.
AC Q9FUU6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Granule bound starch synthase I (EC 2.4.1.21).
GN GBSSI.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. CHEYENNE; TISSUE=ENDOSPERM;
RX McCue K.F., Hurkman W.J., Tanaka C.K., Anderson O.D.;
RT "Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum
RT cv. Cheyenne): Molecular Characterization, Developmental Expression,
RT and Homolog Assignment by Differential PCR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286320; AAG27624.1; -.
DR InterPro; IPR001296; Glycosyl-transf_1.
DR Pfam; PF00534; Glycosyl-transf_1.
DR PROSITE; PS00606; B_KETOACYL-SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

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Query Match 49.8%; Score 1380; DB 10; Length 605;
Best Local Similarity 51.5%; Pred. No. 5.4e-86;
Matches 281; Conservative 72; Mismatches 153; Indels 40; Gaps 9;
QY 2 LDIVMAAEVAPWSKTTGGLGVDTGGLPIELVKRGRHVTMTAPRYDQYADAWDTSVVVDIM 61
Db 78 MNLVFCVCAEAPWSKTTGGLGVDTGGLPPMAANGHRVMTISPRYDQYKDAWDTSVVSEIK 137
QY 62 ----GEKRVYFHSIKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNKHRRALFC 117
Db 138 VADEYERVRVHCYKRGVDRVFDHPCFLKVRGKTKYKIGPDAGTDYEDNQLRFSLLC 197
QY 118 KAAIEARVL-----PF--GP-GEDEVFVANDHMSALVPVLLKDEYQPKQFTKAKSVLA 169

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Db 198 QAALAPRILDLNNPFGSPYGEDVVFVVCNDWHTGILLACYLKSNTQSSGIYRTAKVAF 257
QY 170 IHNIAGQRMWEAEAFKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPLTKYTKKI 229
Db 258 IHNISYQGRSFDDFAQLNLPDRFKSDFDIDGYDK-----PVGE---RKT 300
QY 230 NWLKGGLIAADKLVTPSPNATEIAADAAGVVELDTVIRAKGTGIVNGMDIEBNPKTD 289
Db 301 NWKAGILQADKLVTPSPNATEIAADAAGVVELDTVIRAKGTGIVNGMDIEBNPKTD 360
QY 290 KFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEOKGVDIILAAAPKI 349
Db 361 KFLAANYDVTVALEGRALNEALQAEVGLPVDKRVPLVAFVIGRLEOKGVDVMAALPEI 420
QY 350 LATPKVQIATLGTGKAAEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
Db 421 LKEDVQVILGTGKKEFELLSVEKFFSKVAVVRFNAPLAHQMGADGVLAVTSRF 480
QY 410 EPCGLIQLHAMHYGTVPVVAASSTGLVDTVKGVTFHMGALNP--KLDEADADALAATV 467
Db 481 EPCGLIQLQMGRYGTPCACASTGGLVDTIMEGKTGFHMGHLSVDCNVVPEADVKVVTIL 540
QY 468 RRASEVPAGRYPEMVANCIQSOLSWKPAQKKEGLEEV-----VYKGGVATAKK 519
Db 541 KRAVKVGTTPAYHEMVKNCMIQDLSWRKPAKNWEDVILLEGVGESEPGVIGE-BIAPLAM 599
QY 520 EEIKVP 525
Db 600 ENVAAP 605

RESULT 14
Q9SQ58 PRELIMINARY; PRT; 599 AA.
ID Q9SQ58
AC Q9SQ58;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Granule-bound starch synthase GBSSII.
OS Triticum aestivum (Wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura T., Vrinten P.; to the EMBL/GenBank/DBJ databases.
RL EMBL; AF109395; AAF14233.1; -.
DR InterPro; IPR001296; Glycosyl_transf_1.
DR Pfam; PF00534; Glycosyl_transf_1; 1.
SQ SEQUENCE 599 AA; 66045 MW; D486EFC90557F131 CRC64;

Query Match 49.8%; Score 1379; DB 10; Length 599;
Best Local Similarity 50.4%; Pred. No. 63e-86;
Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;

QY 2 LDIYVAAEAPVPSKGTGGVGTGGLPIELVLRGHRVMTIAPRYDQYADAWDTSVVVDIM 61
Db 72 MPILFATEVHPWCKTGGVGTGGLPVALAAMGHRVMTIAPRYDQYKDTWDTNVLVEVI 131
QY 62 ---GEKVRYPHSTKGGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLHNKRFALFC 117
Db 132 VGDRTETVRFFHCYKRGVDRVDFHPMELEKRVWGTGSKLYGPTGTDFRDNQLRFLC 191
QY 118 KAAIEAARVLPF-----GP-GEDEVFANDWHSALVPLLLKDEYQKQFTKAKSVLA 169
Db 192 LAALAPRVNLNNSYFSGYGENVVFANDWHTAVLPCLYKSMYKONGIYVNAKAVFC 251
QY 170 IHNIAGQRMWEAEAFKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPLTKYTKKI 229
Db 252 IHNIAGQRFPRVDFELLNLPSPMPSPDFDVGHVK-----PVVG---RKT 294

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QY 230 NWLKGGLIAADKLVTPSPNATEIAADAAGVVELDTVIRAKGTGIVNGMDIEBNPKT 288
Db 295 NWKAGITCEDVLTIVSPHYVKELTSGPEKVELDGLVRAKPLETIGVNGMDVVDWNPAT 354
QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEOKGVDIILAAAPK 348
Db 355 DKYTSVKNATTVAAERALNKEILQAEVGLPVDSSIPVIVFVIGRLEOKGSDIILAAIPE 414
QY 349 ILATPKVQIATLGTGKAAEKLVAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSR 408
Db 415 FL-BENVQIIVLGTGKKEEELMLEAKYQNRAGIAKFNVPPLAHMFAAGIIVPSR 473
QY 409 FEPGLIQLHAMHYGTVPVVAASSTGLVDTVKGVTFHMGALNP--DKLDEADADALAAT 466
Db 474 FEPGLIQLQMGRYGTPICSSITGGLVDTVSEGVTFHMGFSNFYEFETVDDPADVAASVN 533
QY 467 VRRASEVPAGRYPEMVANCIQSOLSWKPAQKKEGLEEVVYKGG-----GVA 515
Db 534 VTRAKQYKTPSFHAMVONCMQAQDLSWKGPAAKW----EALLGLGVGSGQPIEGEIEA 589
QY 516 TAKKEEIKVP 525
Db 590 PLAKQNVATP 599

RESULT 15
Q43012 PRELIMINARY; PRT; 606 AA.
ID Q43012
AC Q43012;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Starch granule-bound starch synthase (EC 2.4.1.11).
GN WAXY.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SSP. L.F. SPONTANEA;
RA Hong Z.Y., Zheng F.Q., Gao J.P., Wang X.C., Wu M., Zhang J.L.,
RA Wang M.M.;
RT *Identification of two transposon-like elements in rice wx gene.*;
RL Sci. China B 37:437-447(1994).
DR EMBL; X64108; CAA45472.1; -.
DR InterPro; IPR001296; Glycosyl_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycosyl_transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR Glycosyltransferase; Transferase.
SQ SEQUENCE 606 AA; 66323 MW; E1157468A5553CE CRC64;

Query Match 49.7%; Score 1376; DB 10; Length 606;
Best Local Similarity 50.7%; Pred. No. 1e-85;
Matches 277; Conservative 77; Mismatches 148; Indels 44; Gaps 10;

QY 2 LDIYVAAEAPVPSKGTGGVGTGGLPIELVLRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKGTGGVGTGGLPVALAAMGHRVMTISPRYDQYKDAWDTSVVAEIK 142
QY 61 ---MGEKVRYPHSTKGGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLHNKRFALFC 117
Db 143 VADRTETVRFFHCYKRGVDRVDFIDHPSFLEKRVWGTGSKLYGPTGTDFRDNQLRFLC 202
QY 118 KAAIEAARVLPF-----PEGP---GEDEVFANDWHSALVPLLLKDEYQKQFTKAKSVLA 169
Db 203 Q---EAPRLINLNNPYFKGTGVDVVFVNCNDWHTGILPCLYKNNYKNGIYVNAKAVFC 259
QY 170 IHNIAGQRMWEAEAFKDTKLPOAAFDKLAESDGYAKVYTEATPMEDEKPLTKYTKKI 229
Db 260 IHNISYQGRFAFEDYPELNLSEKSSDFIDGY-----DTPVEG-----RKT 302

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QY	230	NWLKGGIIAADKLVTVSPNYATIAADAAAGGVELDIVIRAKGIEGIVNGMDIEENPKTD	289
Db	303	NWMAKIGIESDRVLTVSPYYAEELISGIARGCELDNIMRLTGITGIVNGMDVSWDFSKD	362
QY	290	KFLSADYDONSVYAGKAAAKEALQAEGLPVDPPTAFITGRLEEQGVDIILAALPKI	349
Db	363	KYVITTYDATTAEAKALNKEALQAEAGLPVDRKVPLIAFTIGRLEEKGQPDVMAAIPEL	422
QY	350	LATPKVQIALILGKGKAAEKLVAIGTKYKGRAGVVKFSAPIAHMTAGADFMLVPSRF	409
Db	423	M-QENVYIVLLGTGKKFKELLKSMEEKYKGVRAVVKFNAPLAHLTMAGADVLAVPSRF	481
QY	410	EPCGLIOLHAMHYGTVPVVASTGGLVDTVKEGTVGFHMGALNPD--KLDERADADALAAIV	467
Db	482	EPCGLIQLQGMRYGTFCACASTGGLVDTVLEGKTGFHMGRLSDCKYVPSFVQKVAITLL	541
QY	468	RRASEYFAGGRYPMEVANCISQDLSKSPKQAKWEGLL-----EBWYVGKGGVAAAKK	519
Db	542	KRAIKIVGTPAYNEMRYNMCNQDLSWKGPAPKNWENVLGLGVAGSEPCVEGE-ETAPLAK	600
QY	520	EEIKVP	525
Db	601	ENVAAP	606

Search completed: June 4, 2003, 14:56:10  
Job time : 30.3807 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 4, 2003, 14:49:26 ; Search time 9.44713 Seconds  
(without alignments)  
1653.790 Million cell updates/sec

Title: US-09-980-771A-9  
Perfect score: 2769  
Sequence: 1 ALDIWVAEAPVWSKTGGL.....GGVATKKEIKVPVAKIP 531

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA: \*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep: \*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1397.5	50.5	609	3	US-08-941-445A-7	Sequence 7, Appli
2	1360.5	49.1	600	4	US-09-388-743-22	Sequence 22, Appl
3	1353.5	48.9	533	3	US-08-941-445A-5	Sequence 5, Appli
4	1342.5	48.5	616	4	US-09-388-743-14	Sequence 14, Appl
5	1315	47.5	614	4	US-09-388-743-18	Sequence 18, Appl
6	1314.5	47.5	615	4	US-09-388-743-2	Sequence 2, Appli
7	902.5	32.6	641	4	US-08-836-567-10	Sequence 10, Appl
8	882.5	31.9	649	4	US-09-192-909-2	Sequence 2, Appli
9	878	31.7	671	4	US-09-196-390-2	Sequence 2, Appli
10	873	31.5	801	4	US-09-388-743-26	Sequence 26, Appl
11	871	31.5	767	4	US-08-836-567-8	Sequence 8, Appli
12	861.5	31.1	539	3	US-08-941-445A-21	Sequence 21, Appl
13	861.5	31.1	583	3	US-08-941-445A-13	Sequence 13, Appl
14	858	31.0	690	4	US-09-388-743-6	Sequence 6, Appli
15	845	30.5	558	4	US-08-836-567-6	Sequence 6, Appli
16	841	30.4	799	4	US-09-196-390-6	Sequence 6, Appli
17	837	30.2	698	3	US-08-941-445A-11	Sequence 11, Appl
18	726	26.2	459	4	US-08-836-567-4	Sequence 4, Appli
19	701.5	25.3	669	3	US-08-941-445A-9	Sequence 9, Appli
20	580	20.9	477	1	US-07-735-065-2	Sequence 2, Appli
21	580	20.9	477	1	US-08-469-202-12	Sequence 12, Appl
22	580	20.9	477	2	US-08-484-434C-12	Sequence 12, Appl
23	568.5	20.5	677	4	US-08-836-567-2	Sequence 2, Appli
24	568.5	20.5	1197	4	US-08-836-567-12	Sequence 12, Appl
25	568.5	20.5	1230	2	US-08-968-542C-35	Sequence 35, Appl
26	545	19.7	735	4	US-09-115-704-2	Sequence 2, Appli
27	530.5	19.2	533	4	US-09-388-743-10	Sequence 10, Appl

28	504	18.2	1674	2	US-08-968-542C-12	Sequence 12, Appli
29	240	8.7	64	2	US-08-470-720-15	Sequence 15, Appl
30	215.5	7.8	79	2	US-08-470-720-13	Sequence 13, Appl
31	143.5	5.2	59	2	US-08-470-720-14	Sequence 14, Appl
32	129	4.7	30	2	US-08-470-720-9	Sequence 9, Appli
33	122	4.4	29	2	US-08-470-720-16	Sequence 16, Appli
34	121	4.4	27	2	US-08-470-720-7	Sequence 7, Appli
35	112	4.0	34	2	US-08-470-720-11	Sequence 11, Appl
36	112	4.0	1037	4	US-09-134-001C-4794	Sequence 4794, Ap
37	108	3.9	701	4	US-09-132-028-2	Sequence 2, Appli
38	107	3.9	69	2	US-08-470-720-6	Sequence 6, Appli
39	107	3.9	111	2	US-08-470-720-18	Sequence 18, Appl
40	105.5	3.8	490	4	US-09-292-225-41	Sequence 41, Appl
41	105.5	3.8	509	4	US-09-292-225-35	Sequence 35, Appl
42	105.5	3.8	509	4	US-09-292-225-38	Sequence 38, Appl
43	104.5	3.8	387	4	US-09-134-001C-3206	Sequence 3206, Ap
44	104	3.8	722	4	US-09-134-001C-5482	Sequence 5482, Ap
45	104	3.8	807	4	US-08-855-910-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-08-941-445A-7  
; Sequence 7, Application US/08941445A  
; Patent No. 6107060  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; APPLICANT: Guan, Hanning  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445A  
; FILING DATE: 30-SEP-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 609 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-941-445A-7

Query Match 50.5%; Score 1397.5; DB 3; Length 609;  
Best Local Similarity 51.4%; Pred. No. 6.7e-134;  
Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;  
QY 2 LDIVWVAEAPVWSKTGGLGVDTGGLPIELVKRGHRYMTAPRYDQYADAMDTSVVYDI- 60  
Db 83 MNVVFVGAEMPNWSKTGGLGVDTGGLPIELVKRGHRYMTAPRYDQYADAMDTSVVYAEIK 142

QY	170	IHNIAFGRMWEAFKDKTLPQAAFDKLPASDGYAKVYVTEATPMEDEKEPPLTGKTYKKI	229
Db	253	IHNMAYQGRFAFPDFSLNLPDFTFKSDFDFGYTK-----PVKG-----RKI	295
QY	230	NWLKGLIIADKLVTVSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEWNPKTD	289
Db	296	NWMAKGLIADKLVTVSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEWNPKTD	355
QY	290	KFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFIRLEEGKGVDIILALPKI	349
Db	356	KFIITANDATMTAKRVNKEQLQAEVGLPVD-PIPIVIVFVGRLEEGKGSIDILAAAIPEL	415
QY	350	LATPKVQIAILGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF	409
Db	416	M-DENVQIILGTGKHLKELEIEEQFPDKMLVAKFVPLAHMMAGGDFIIIPSRF	474
QY	410	EPCGLIQLHAMHYGTVPVWASTGGLVDTKGVGTGFHMGALNPD--KLDEADADALAATV	467
Db	475	EPCGLIQLQGRMYGTPCACASTGGLVDTVIEGKGFHMGRLSVDCKVPEPSDKVKAATL	534
QY	468	RRASEVFAAGGRYPENVANCISQDLSWSKPAQKWEGLEEVVYKGGVATAKKE	520
Db	535	KRALVYGTPTAFSEWVQNCMAQHSWKEPAKKWEELLIGLEVDGSEPGFGEIAPLAKE	594
QY	521	EIKVP	525
Db	595	NVAAP	599
RESULT 3			
US-08-941-445A-5			
; Sequence 5, Application US/08941445A			
; Patent No. 6107060			
; GENERAL INFORMATION:			
; APPLICANT: Keeling, Peter			
; APPLICANT: Guan, Hanping			
; TITLE OF INVENTION: Starch Encapsulation			
; NUMBER OF SEQUENCES: 37			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.			
; STREET: 5370 Manhattan Circle			
; CITY: Boulder			
; STATE: CO			
; COUNTRY: US			
; ZIP: 80303			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/941,445A			
; FILING DATE: 30-SEP-1997			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/026,855			
; FILING DATE: 30-SEP-1996			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Winner, Ellen P			
; REGISTRATION NUMBER: 28,547			
; REFERENCE/DOCKET NUMBER: 89-97			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (303) 499-8080			
; TELEFAX: (303) 499-8089			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 533 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-941-445A-5			

Y	61	---MGEKVYFHSIKKGVHVVWIDHPWELAKVWGKTSKLYGPRSGADYLDNHRKALFC	117	
b	143	VADRYERVRFFHCYKRGVORVFIDHPSLEKVGWKGTEKLYGPDGVYKDNQMRSLLC	202	
Y	118	KAATEARVL-----PFGP----	CEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA	169
b	203	QAALAPRIILNANNPYFKGTGVEDVVCNDWHTGTPLASYLKNNTQPNGLYRNKAVFC	262	
Y	170	IHNIAFGRMWEAFKDKTLPQAAFDKLPASDGYAKVYVTEATPMEDEKEPPLTGKTYKKI	229	
b	263	IHNISYQGRFAFEDYELNLSERFRSFDIDG-----DTPVEG-----	RKI	305
Y	230	NWLKGLIIADKLVTVSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEWNPKTD	289	
b	306	NWMAKGLIADKLVTVSPNYATEIAADAAGGVELDTVIRAKGTGIVNGMDIEWNPKTD	365	
Y	290	KFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLFAFIRLEEGKGVDIILALPKI	349	
b	366	KYITAKYDATTATEAKALKEALQAEAGLPVDRKRIPLIAFIRLEEGKGVDMVMAAIPEL	425	
Y	350	LATPKVQIAILGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF	409	
b	426	M-QEDVQIVLGTGKKEKLLSMEEKYPCKVRVAVVKNAPLAHLIMAGADVLAIVPSRF	484	
Y	410	EPCGLIQLHAMHYGTVPVWASTGGLVDTKGVGTGFHMGALNPD--KLDEADADALAATV	467	
b	485	EPCGLIQLQGRMYGTPCACASTGGLVDTVIEGKGFHMGRLSVDCKVPEPSDKVKAATL	544	
Y	468	RRASEVFAAGGRYPENVANCISQDLSWSKPAQKWEGLEEVVYKGG-----VATAK	518	
b	545	KRALVYGTPTAFSEWVQNCMAQHSWKEPAKKWEELLIGLEVDGSEPGFGEIAPLA	602	
Y	519	KEEKVVP	525	
Db	603	KENVAAP	609	
RESULT 2				
US-09-388-743-22				
; Sequence 22, Application US/09388743				
; Patent No. 6423886				
; GENERAL INFORMATION:				
; APPLICANT: Singletary, George				
; APPLICANT: Zhou, Ian				
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their				
; FILE REFERENCE: 1144				
; CURRENT APPLICATION NUMBER: US/09/388,743				
; CURRENT FILING DATE: 1999-09-02				
; NUMBER OF SEQ ID NOS: 28				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 22				
; LENGTH: 600				
; TYPE: PRT				
; ORGANISM: Tulipa fosteriana				
US-09-388-743-22				
Query Match				
Best Local Similarity 49.1%; Score 1360.5; DB 4; Length 600;				
Matches 272; Conservative 77; Mismatches 157; Indels 39; Gaps 9;				
QY	2	LDIVMVAEAPWSKGTGLDVTGGLPIELVKRHRVMTIAPRYQYADAWPTSVVVDI-	60	
Db	73	MNLVFGTGTGYSKGTGLDVLGPPALAAARGHRVMVTPRYQYKDAWNTVLEIK	132	
QY	61	MEKE---VRYFHSIKKGVHVVWIDHPWELAKVWGKTSKLYGPRSGADYLDNHRKALFC	117	
Db	133	VGDKMETVRFELHKGVRDVFIDHPSLEKVGWKGTEKLYGPDGVYKDNQMRSLLC	192	
QY	118	KAATEARVL-----GP-CECVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA	169	
Db	193	QAALAPRIILNANNPYFKGTGVEDVVCNDWHTGTPLASYLKNNTQPNGLYRNKAVFC	252	



QY 170 IHNIAGQRMWEEAFKDTKLPQAAFDKLAFLSDGAKYVTEATPMEDEKPPILTKYKKI 229  
Db 268 IHNISQGRFSDFEFLNLPENFKSFSFIDGYNK-----PVKG---MKI 310  
QY 230 NMLKGGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRAKGLEGTIVGMDIEWPKTD 289  
Db 311 NNMKAGILESDRVFTVSPYQAELLGSEERGVLDNLRVTSTITGIVGMDVNEWNP LTD 370  
QY 290 KELSAPYDONSIVYAGKAARKEALQALGLPVDPTAPLFAFICGLEKQKGVDIILALPKI 349  
Db 371 KYISVNDKAPVMEAKPLNKEALQALGLPVDPTAPLFAFICGLEKQKGVDIILALPKI 430  
QY 350 LAPPKVOIATLGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSRF 409  
Db 431 M-DENVQLIILGTGKKEMENQLESMEEMFDPKVRVNMKFNAPLAHQMTAGADIIVIPSRF 489  
QY 410 EPCGLIQLHAMHYGTVVPVASTGGLVDTVKEGVTGFMHGALNP--DKLDEADADALAATV 467  
Db 490 EPCGLIQLQCMQYGTPTSACSTGGLVDTVKEGVTGFMHGPFSAFCEVVDLSLVKKVVITY 549  
QY 468 BRASEVPAGGRYPPEMVANVCISODLSWSKPAQKWEGLL-----EYVYKGGVATAK 523  
Db 550 KRLKVIYGTAPFEMTQNCMAQDLSWKGPAKNEQVLLNL-----GVAGSEPGYDGEI- 603  
QY 524 VPVAEK 529  
Db 604 VPLAKE 609

RESULT 6  
US-09-388-743-2  
; Sequence 2, Application US/09388743  
; Patent No. 6423886  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Lan  
; TITLE OF INVENTION: No. 6423886a1 Starch Synthase Polynucleotides and Their  
; TITLE OF INVENTION: Use in the Production of New Starches  
; FILE REFERENCE: 1144  
; CURRENT APPLICATION NUMBER: US/09/388,743  
; NUMBER OF SEQ ID NOS: 28  
; CURRENT FILING DATE: 1999-09-02  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Curcuma zedoaria  
US-09-388-743-2

Query Match 47.5%; Score 1314.5; DB 4; Length 615;  
Best Local Similarity 49.5%; Pred. No. 2.1e-125;  
Matches 271; Conservative 76; Mismatches 157; Indels 43; Gaps 12;  
QY 2 LDIVWAAEVAPWSKTGSLGDTGCLPIELVKRHRVMTIAPRYDQYADAWTTSVVVDI- 60  
Db 89 MNLIFVAEAVAPWSKTGSLGDTGCLPPAMAKRHRVMTIAPRHQYKDGWDVAVFVLEK 148  
QY 61 MG---EKVRYTHS IKKGVRHYWDHPFLAKVWGTGSKLYGPRSGADYLDNKRFPALFC 117  
Db 149 VGDRIETVRFHCYKRGVDRVFDPLFLEKVGWGTGGKIYGPVTFDYEDNQLRFLC 208  
QY 118 KAAIEAARYL-----PFGP-GEDCVFVANDWHSALVPVLKD-EYQPKGQFTAKSVL 168  
Db 209 LATLETPTVPLNPNNNKYHSGPKGED-LETANDWHTALLPCYLKTTIVYQAHGYKNAKAVF 267  
QY 169 AIHNTAFQGRWEEAFKDTKLPQAAFDKLAFLSDGAKYVTEATPMEDEKPPILTKYKKI 228  
Db 268 CIHNTAYQGRFAFEDFSRLNLPDTEFKSFDIDGYAK-----PIKG---RK 310  
QY 229 INWLKGGIITAAKLVTVSPNYATEIAADAAGGVDELTVIRAKGLEGTIVGMDIEWNPXT 288  
Db 311 INNMKAGIIESRALTVSPYQAELLGSEERGVLDNLRVTSTITGIVGMDVNEWNPST 370

QY 289 DKFLSAPYDONSIVYAGKAARKEALQALGLPVDPTAPLFAFICGLEKQKGVDIILALPK 348  
Db 371 DKVITYADTTWEAKPLNKEALQALGLPVDPTAPLFAFICGLEKQKGVDIILALPK 430  
QY 349 ILATPQVOIALGTGKAAYEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSR 408  
Db 431 FF-DQDVQVIVLGTGKKLERQALLDEDFDKRAHMKFNIPLAHIMAGADIIIVIPSR 489  
QY 409 FEPCLGLIQLHAMHYGTVVPVASTGGLVDTVKEGVTGFMHG--ALNPKLDEADADALAAT 466  
Db 490 FEPCLGLIQLQCMRYGTPTSMTCTTGGVLDVTKEGITGFMHGPFSAFCEVVDLSLVK 549  
QY 467 VRASEVPAGGRYPPEMVANVCISODLSWSKPAQKWEGLL-----EYVYKGGVATAK 518  
Db 550 VKRALMVIYGTAPFEMTQNCMAQDLSWKGPAKNEQVLLNL-----GVAGSEPGYDGEI- 608  
QY 519 KEEIKVP 525  
Db 609 KENVATP 615

RESULT 7  
US-08-836-567-10  
; Sequence 10, Application US/08836567  
; Patent No. 6130367  
; GENERAL INFORMATION:  
; APPLICANT: Kossmann, Jens  
; APPLICANT: Springer, Franziska  
; APPLICANT: Abel, Gernot  
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/836,567  
; FILING DATE: 24-JUL-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/04415  
; FILING DATE: 09-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 44 41 408.0  
; FILING DATE: 10-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Agrevo-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 641 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-836-567-10

Query Match 32.6%; Score 902.5; DB 4; Length 641;  
Best Local Similarity 39.8%; Pred. No. 2.8e-83;  
Matches 212; Conservative 90; Mismatches 161; Indels 69; Gaps 19;



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3 DIVVAAFPVAPWSKTGGGLDVTGGLPIELVKRGHRVMTIAPRY-----DOYADAWDTS 55
132 NIIETWAAAPYSKTGGGLDVCGLSPMLAARAGHRVNVVSPRYLNGGSPDEKGYANAVDLD 191
56 V--VVDIING--EKVRYPHSIIKKGVHRVWIDHPWFLAKVWGKTGSKLYSPRGSDAYIDNHK 111
192 VRATVHCFGAQAEVAFHEYRAGVDWVEVDHSSYC-----RPGTP-YGDIYGA-FGDNQF 244
112 RFALFCKAATFAARVLPFGP--GEDCVFVANDHSAIPLVLLKDEYQPKGQFTRAKSYL 168
245 RFTLLSHAACAPLVLPLGGFTYGEKCLFLANDHAALVPLLLAAKRYPGYVYKQARSIV 304
169 AIHNIAFQGRMEAEAFKDTKLUPAAFDKLAISDGYAKVYTEATPMEDEKPLPTGKTYK 228
305 AIHNIAHQGVEPATYNNLGPLPQWYGAV---EWIFTPWARAHLD-----TGET--- 351
229 INMLKGIILAADKLVTVSPNATYATFAADAAGVELDVTVI--RAKIGIEVINGMDTEWNP 286
352 VNYLKGAIAVADRILTVTSQGSWEIIT-PEGYGLHELLSSRQSVLNGITNGIDVNDNP 410
287 KTKELFASPDQNSVYAKKAARAKALQAEGLPVDPTAPLFAFIRGLEBEQGVDIILAL 346
411 STDEHTASHYSINDL-SGKVCQKTDLOKELGLRTPDCPLGIFGLRDLYQKGVDIILSAI 469
347 PKLITATPKVQITAILGTGKAAYEKLNVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVP 406
470 PELMQN-DVQVVMLGSEKQYEDWMRHTENLFKOKFRAGVGNFVPSHRITAGCDILLMP 528
407 SRPEPGCGLIQLHAMHYGTVPVWASTGGGLVDTVK-----EGV---TGFHMGALNPDKLD 456
529 SRPEPGCLNQLYAMRYGTIPIVHSTGGLRDIVKDFNPYAQBSGIGEGTGWTSPLTSEKL- 587
457 EADADALAAIVRASEWFAAGRTP-----MVANCIQDLSWSKSPAQKWE 501
588 ---LDTLKLAI-----GTTEHKSSWEGLMRRGMGRDYSWENAAIOYF 627

```

RESULT 8  
US-09-192-909-2  
; Sequence 2, Application US/09192909  
; Patent No. 6307124  
; GENERAL INFORMATION:  
; APPLICANT: Jens Kossmann  
; APPLICANT: Claus Froberg  
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble  
; TITLE OF INVENTION: starch synthases from maize  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/192,909  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP97/02527  
; FILING DATE: 16-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 19 918.2  
; FILING DATE: 17-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794

```

; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 649 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-192-909-2

Query Match 31.9%; Score 882.5; DB 4; Length 649;
Best Local Similarity 38.4%; Pred. No. 3.2e-81;
Matches 203; Conservative 95; Mismatches 174; Indels 57; Gaps 15

QY      3 DIVVVAEAVPWSKTGGIGDVTGGPIELIVKGRHVMITADRY-----DQYADAWDTSV 56
Db      142 NIVFTGASPYAKSGGLGDCGSLPALAARGHRVVMVMPRLNGTSDKNYANAFYTEK 201
QY      57 VVDIM--GE-KVRYFSHKKGVRHVDHPFLAKVWGKTGSKLYGPRSGADYLDNHRK 112
Db      202 HIRPCFGGEHEVTFEYHRVSVDWVFVDHSY-----HRPENLYGDKFGA-FGDNQPR 254
QY      113 FALPCKAAIEARVLPPGP----GDCVFVANDWHSALVPVLKDEYQPKGQFTKAKSVLA 169
Db      255 YTLCLYAAACEAPLLELGGYTYGQCMFVWNDWHSALVPVLLAAKYRYPGVYKDSRLV 314
QY      170 IHNIAFGRMWEEAFKTKLPQAAFDKLFASDGYAKYVTEATPMEDEKPPLTGTYKKI 229
Db      315 IHNIAHGVGPASTYDPLGLPPEWYGALW-----VEPEARRHALDKG-----EAV 361
QY      230 NWLKGGIIAADKLVTVPNTATEATAADAGGVELDTVI--RAKGTEGVINGMDIEENPK 287
Db      362 NELKGAVVADRIYTVSKGSWEVTT-AEGGQGLNELSSRKSVLGVINGIDINDWNP 420
QY      288 TDKFLSAPYDONSVYAGAAAKEALQALGLPVDPTAPLFAFIGLEBQKGVDIITLALP 347
Db      421 TDKCIPCHYSVDLL-SGKAKCKGALQELGLPIRPDPVPLIGFIELDYQKGLDLQLIP 479
QY      348 KILATPKVQIATLGTGAAAEKLVNATGTYKGRAGKGVVKSAPLAHMLTAGADEMLVPS 407
Db      480 DLM-REDVQVFMVGSGDPELMDWMRKSTESIFKDKFERGVWGFVSPVSHRITAGCDILLMP 538
QY      408 RFEPGGLIQLHAMHYGVPPVVAASVGGVLIVTK-----EGVTGFHMGALNPKLDEA 458
Db      539 RFEPGGLNQLYAMQYGVVPPVHAITGGLRDVTVENPFGENCEQGTGWAFAPLTEN---- 594
QY      459 DADALAATVRRSEVFAGGR--YPMVANCISQDLSWSKPAQKWEGLLE 505
Db      595 ----MLWTLRTALSTYREHKSWSGLMKRGMKSGKFTWDAHAAEOYEOFTO 639

```

RESULT 9  
 US-9-196-390-2  
 ; Sequence 2, Application US/09196390  
 ; Patent No. 6307125  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Block, Martina  
 ; APPLICANT: Lorz, Horst  
 ; APPLICANT: Lutticke, Stephanie  
 ; APPLICANT: Walter, Lennart  
 ; APPLICANT: Froberg, Claus  
 ; APPLICANT: Kossmann, Jens  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
 ; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH  
 ; TITLE OF INVENTION: SYNTHESIS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York



```

; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCI/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agreevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 767 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-567-8

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Query Match 31.5%; Score 871; DB 4; Length 767;
Best Local Similarity 39.7%; Pred. No. 6.2e-80;
Matches 210; Conservative 78; Mismatches 181; Indels 60; Gaps 14;

QY 2 LDIVVAAEVAWPSKGTGLGDTGGTGLPIELVKGHRVMTIAPRYDOYADAWDSV---V 57
DB 276 MNIIVASECAPWSKGTGLGDTGGTGLPIELVKGHRVMTIAPRYDOYADAWDSV---V 57
QY 58 VDIMGEKVYFHSIKKGVHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHNKRFALFC 117
DB 336 VDGQVVEITYFQAFIDGVDFVFD-----SHMFRHIGNNIY-----GGRVVDILKRVVLF 386
QY 118 KAAIEAARVLP-----FGPCEDCVFVANDWHSALVPLVLLKDEYOPKGOFTKAKSVLAHN 172
DB 387 KAAIEVPWHPVCGVCYGDG-NLVFTANDWHTALLPYLKAYTRDNGIMNTRSVLIHN 445
QY 173 IAPQGRWEEAEKDTKLPAQAFDKLAFSDGYAKVYVTEATPMEDEKPLTGTGYKKINWL 232
DB 446 IAHQGRGLDFSFYVDLPVPHYMDPKLYD-----PVCGEHF---NIF 484
QY 233 KGGIIADKLVTYSPNKAIEAADAAGVDELTVIRAKG---IEGIWGMDEIEWNPKTDK 290
DB 485 AAGLKATADVTVVSHGYSWELKT-SQGGWGLHOIINENDWKLQIYNGIDTKWNPELD 543
QY 291 FLISAP-----YDONSVYVAGAAKAEALQAEGLPDPDTAPLFAFIEGLEQKGVDDIILAL 346
DB 544 HLQSDGYMYSLDTLQGTQPKCAQALQKELGULPVRDVPVLIIGFIDLPQKGVDDIILAEAS 603
QY 347 PKILATPKVQIAILLGTGKAAEKLVAIGTKYGRKGVVKSAPLAHMLTAGADFWIYP 406

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DB 604 ANMMG-QDVQLVMLGTGRDLQMLRFQECQHNDKIRGWGFSVKTSHRITAGADILLMP 662
QY 407 SRFECGLIQLHAMVGTVPVVASVGGGLVDTVK-----EGVTGFHMGALNPKDLDEADA 460
DB 663 SRFECGGLNQLYAMKIYIIPVHVAVGGLRDITVQFPDFNFESGLIGWTFSRAEASQLIHG 722
QY 461 DALAATVRRASEVVFAGGRYPENVANCISODLSWSKPAQKWEGLLEVVY 509
DB 723 NCL-LTYREYKKSWE-----IQTRMTODLSWDNAAQNYEVLIAKY 765

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## RESULT 12

```

US-08-941-445A-21
; Sequence 21, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-941-445A-21

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Query Match 31.1%; Score 861.5; DB 3; Length 539;
Best Local Similarity 40.8%; Pred. No. 3.2e-79;
Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;

QY 4 IVVVAEVAWPSKGTGLGDTGGTGLPIELVKGHRVMTIAPRY-----DOYADAWDSV 57
DB 51 IVFTGTGASPYAKSGGLGDTGGTGLPVALAARGHRVVMVMPRYLNGTSDKNYANAFYTEKH 110
QY 58 VDIM--GE-KVRYFHSIKKGVHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHNKRF 113
DB 111 IRPCPGGEHEVTFEYRDSVDVWFVDHPSY-----HRPGNLYGDKFGA-FGDQF 163
QY 114 ALFCAAEIAEARVLPFGP---GEDCVFVANDWHSALVPLVLLKDEYOPKGOFTKAKSVLA 170
DB 164 TLACYAACEAPLILELGGIYQNCMFVNDWHSALVPLVLLAKYRPYGVYKDSRLVI 223
QY 171 HNTAFQGRWEEAEKDTKLPAQAFDKLAFSDGYAKVYVTEATPMEDEKPLTGTGYKKIN 230

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Db 224 HNLHQGVPEASTYDGLGLPPEWYGALWE-----VFPWARHRLDKG-----EAVN 270
QY 231 WLKGGIIAADKLVTSPTYATEIAADAAGGVLDTVI--RAKIEGIVNGMDIEEWNPKT 288
Db 271 FLKGAVVATADRIIVTSKGSWEVTT-AEGGQGLNELLSSRKSVLNGVINGIDINDWNPAT 329
QY 289 DKFLSAPYDQNSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAALEPK 348
Db 330 DKCIPCHYSVDDL-SGKAKCKGALQKELGLPIRPDVPPLIGFIRGLDYQKGDILQLIIPD 388
QY 349 ILATPKVQIATLGTGKAAEKEKLVNAIGTKYKGRAGKGVVKSAPLAHMLTAGADFMVLPSP 408
Db 389 LM-REDVQVFMGLSGDPELEDWMRSTESIFDKFRGWGFSVPVSHRITAGCDILLMPSP 447
QY 409 FEPCCGLIQLHAMHYGTVPVVASTGGGLVDTVK-----EGVTGFHMGALNPKDL 455
Db 448 FEPCCGLNQLYAMQYGTVPVVAHATGGURDITVENFPFGENGEGQGTGWAFAPLITENN 503

RESULT 13
US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-941-445A-13

Query Match 31.1%; Score 861.5; DB 3; Length 583;
Best Local Similarity 40.8%; Pred. No. 3.7e-79;
Matches 194; Conservative 81; Mismatches 154; Indels 47; Gaps 13;

QY 4 IVMVAEAVAPSKTGGGLDVTGGLPIELVKRGHRVMTIAPRY--KGIEGIVNGMDIEEWNPKT 57
Db 95 IVFVTGEASPYAKSGGLGDCVGLPVALAARGHRVMTIAPRYNGTSDKNYANAFYTEKH 154
QY 58 VDIM--GE-KVRYPHSTIKKGVRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRFR 113
Db 155 IRIPCFGGEHEVTFEYRDSVDWVFDHPSY-----HRPGLNYGDKFGA-FGDNQFRY 207
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QY 114 ALFCKAAIIPAAARVLPFGP---GEDCVFVANDWESALVPVLLKDEYQPKGFTKAKSVLAI 170
Db 208 TLCLYAAACEAPLILELGGYIYQNCMFVVDWFEASLPVLLAAKYRYPYGVYKDSRSILVI 267
QY 171 HNTAFQGRWWEFAFKTKLPQAAFDKLAFSDDGYAKVYVTEATPWEDEKPELTKTKYKKN 230
Db 268 HNLHQGVPEASTYDGLGLPPEWYGALWE-----VFPWARHRLDKG-----EAVN 314
QY 231 WLKGGIIAADKLVTSPTYATEIAADAAGGVLDTVI--RAKIEGIVNGMDIEEWNPKT 288
Db 315 FLKGAVVATADRIIVTSKGSWEVTT-AEGGQGLNELLSSRKSVLNGVINGIDINDWNPAT 373
QY 289 DKFLSAPYDQNSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAALEPK 348
Db 374 DKCIPCHYSVDDL-SGKAKCKGALQKELGLPIRPDVPPLIGFIRGLDYQKGDILQLIIPD 432
QY 349 ILATPKVQIATLGTGKAAEKEKLVNAIGTKYKGRAGKGVVKSAPLAHMLTAGADFMVLPSP 408
Db 433 LM-REDVQVFMGLSGDPELEDWMRSTESIFDKFRGWGFSVPVSHRITAGCDILLMPSP 491
QY 409 FEPCCGLIQLHAMHYGTVPVVASTGGGLVDTVK-----EGVTGFHMGALNPKDL 455
Db 492 FEPCCGLNQLYAMQYGTVPVVAHATGGURDITVENFPFGENGEGQGTGWAFAPLITENN 547

RESULT 14
US-09-388-743-6
; Sequence 6, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their
; FILE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Curcuma zedoaria
US-09-388-743-6

Query Match 31.0%; Score 858; DB 4; Length 690;
Best Local Similarity 39.0%; Pred. No. 1.1e-78;
Matches 208; Conservative 80; Mismatches 176; Indels 70; Gaps 15;

QY 2 LDIVVAAEAVAPSKTGGGLDVTGGLPIELVKRGHRVMTIAPRYDOYADADMTSVV---- 57
Db 199 MNILVAEAPSKTGGGLDVTGGLPVALAKALAKRGHRVMTIAPRYDOYADADMTSVV---- 258
QY 58 VDINGEKVRYPHSTIKKGVRVWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRKRFALFC 117
Db 259 VDGQDMELKYYTHYIDSDVFIDSP-----IFRIGNDIY----GGNRVDILKEMVLF 309
QY 118 KAAIEAARVLP-----FGPGEDEVFVANDWESALVPVLLKDEYQPKGFTKAKSVLAIHN 172
Db 310 KAAVEVPWHVPCGGFCYGDG-NLVFIANDWHTSLPVPVYLKACFRDRGLMTYARCILLVHN 368
QY 173 IAFQGRWWEFAFKTKLPQAAFDKLAFSDDGYAKVYVTEATPWEDEKPELTKTKYKKNWL 232
Db 369 IAHQGRPLDDSFVYVDLPHDLIDSPRDD-----PVGSEHF---NLF 407
QY 233 KGGIIAADKLVTSPTYATEIAADAAGGVLDTVI--RAKIEGIVNGMDIEEWNPKT 290
Db 408 AAGTAAADRVTVSHGYAWELKT-SEGCGWGLFEIINECHWKPFHGVINGIDTSHWNPKEA 466
QY 291 FLSAP-----YDQNSVYAGKAAKAEALQALGLPVDPTAPLFAFIRLEEQKGVDIILAA 346
Db 467 HLNSDGYNTFTLETLEMGKAOCKAALQREFGLPVRDDVPILAFIRGLDHQKGDILTAAM 526
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:56:21 ; Search time 16.3988 seconds  
(without alignments)  
3342.965 Million cell updates/sec

Title: US-09-980-771A-9  
Perfect score: 2769  
Sequence: 1 ALDIVMAAEVAPWSKTGGL.....GGVATAKEELKVPVAKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCI\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1450.5	52.4	636	9	US-10-138-075-4
2	1433.5	51.8	609	9	US-10-138-075-2
3	1379	49.8	599	9	US-10-138-075-5
4	878	31.7	671	10	US-09-952-677-2
5	841	30.4	799	10	US-09-952-677-6
6	555	20.0	915	9	US-10-163-214-6
7	549	19.8	914	9	US-10-163-214-12
8	545	19.7	909	9	US-10-163-214-2
9	537	19.4	874	9	US-10-163-214-13
10	410.5	14.8	474	12	US-10-007-693-99
11	402.5	14.5	476	12	US-10-007-693-69
12	385.5	13.9	293	9	US-10-163-214-10
13	215.5	7.8	117	10	US-09-739-438-2
14	206	7.4	409	9	US-09-738-626-4738
15	189	6.8	381	9	US-09-738-626-5896
16	164	5.9	143	10	US-09-739-438-4
17	155.5	5.6	191	10	US-09-924-358-22
18	155.5	5.6	418	9	US-09-738-626-3951
19	136.5	4.9	385	10	US-09-767-041-18

20	126	4.6	387	9	US-09-738-626-3890	Sequence 3890, Ap
21	125.5	4.5	398	10	US-09-934-899-16	Sequence 16, Appl
22	125.5	4.5	398	10	US-09-934-868-36	Sequence 36, Appl
23	124	4.5	379	9	US-09-738-626-6655	Sequence 6655, Ap
24	123.5	4.5	413	9	US-09-738-626-4025	Sequence 4025, Ap
25	118.5	4.3	372	10	US-09-815-242-5277	Sequence 5277, Ap
26	118.5	4.3	384	10	US-09-815-242-12605	Sequence 12605, A
27	117.5	4.2	636	9	US-09-738-626-5590	Sequence 5590, Ap
28	114.5	4.1	2993	9	US-09-738-626-6239	Sequence 6239, Ap
29	110.5	4.0	121	9	US-10-163-214-4	Sequence 4, Appli
30	108	3.9	802	9	US-10-080-114A-2	Sequence 2, Appli
31	108	3.9	809	9	US-10-080-114A-12	Sequence 12, Appli
32	106	3.8	718	10	US-09-815-242-12915	Sequence 12915, A
33	106	3.8	802	9	US-10-080-114A-5	Sequence 5, Appli
34	105.5	3.8	490	9	US-10-218-743-41	Sequence 41, Appl
35	105.5	3.8	509	9	US-10-218-743-35	Sequence 35, Appl
36	105.5	3.8	509	9	US-10-218-743-38	Sequence 38, Appl
37	105.5	3.8	1156	10	US-09-815-242-13187	Sequence 13187, A
38	105	3.8	195	10	US-09-815-028-8	Sequence 8, Appli
39	104.5	3.8	732	10	US-09-381-624A-3	Sequence 3, Appli
40	102.5	3.7	489	10	US-09-815-242-11953	Sequence 11953, A
41	102.5	3.7	805	9	US-10-137-036-77	Sequence 77, Appl
42	102	3.7	3816	9	US-09-808-880-3	Sequence 3, Appli
43	101.5	3.7	1164	10	US-09-870-122-1	Sequence 1, Appli
44	99	3.6	562	9	US-09-712-363-254	Sequence 254, App
45	98.5	3.6	448	9	US-09-738-626-3991	Sequence 3991, Ap

## ALIGNMENTS

## RESULT 1

US-10-138-075-4  
; Sequence 4, Application US/10138075  
; Publication No. US20030087369A1  
; GENERAL INFORMATION:  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Karlene H.  
; APPLICANT: Harvell, Leslie T.  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Orozco, Emil M.  
; TITLE OF INVENTION: Granule-Bound Starch Synthase  
; FILE REFERENCE: BRL474 NA  
; CURRENT APPLICATION NUMBER: US/10/138,075  
; PRIOR FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/288,315  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 4  
; LENGTH: 636  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-138-075-4

Query Match	52.4%	Score 1450.5;	DB 9;	Length 636;
Best Local Similarity	53.0%	Pred. No. 6.3e-113;		
Matches 291;	Conservative	71;	Mismatches 144;	Indels 43; Gaps 10;
QY	2	LDIVMAAEVAPWSKTGGLGVGGGLPIELVVKGRHVTIAPRYDOYADAMDTSVVYDI-	60	
Db	106	MTFIITGTEVAPWCKTGGLGVGGGLPPALAGFGRHVTIAPRYDOYADAMDTSVVLEVK	165	
QY	61	--MGEKRVFHSITKGVHRVWIDHPWFLAKVWCKTSGKLYGPRSGADYLDNKKRFLFC	117	
Db	166	VGRTKRVFHCYKRGVDRVFDHPWFLKGVWCKTSGKLYGPRSGADYLDNKKRFLFC	225	
QY	118	KAAIEAARVLPPF-----GP-GEDCVFVANDHSAALVPVLLKDEYQPKGQFTKAKSVLA	169	
Db	226	QAALEAPRVLSSNLSKYFSGPYGEDYIFVANDHNTALIFCYLKSMTQSGRIYTNARVVF	285	
QY	170	IHNIAQGRWEAFKDTKLPOAFAFKLAFSDGAKVYTEATPMEDEKPLFGKTYKKI	229	

Db 286 IHNIAYQGRFAFADEFSLILNPQKSSFDIDGHVK-----PVVG---RKI 328  
QY 230 NWLKGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRA-----KGIEGIVNGMOTEEWN 285  
Db 329 NWLKGIIIESWVITVSPNYAKELVSGPKGVDELNIIIRKIDDDGRLVGIIVNGMDVQEN 388  
QY 286 PKTDKPLSAPYQNSYAGKAAKALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAA 345  
Db 389 PITDKVIKYDVSTVLEAKKALKEALQAEVGLPVDNIPNLGIFGRLSEOKGSDILAEA 448  
QY 346 LPKILATPKVQIAILGTGAAYEKUNAGTKYKGRAGKGVVKSAPLAHMLTAGADPMLV 405  
Db 449 IPOFI-KONVQLVALGTGKQKMLELEISYPPDKARGVAKFNVPLAHMIIAGADFILV 507  
QY 406 PSRFEPCGLIOLHAMHYGVPPVASTGGGLVDIVTKEGVTGFHMGALNP--DKLDEADADAL 463  
Db 508 PSRFEPCGLIOLQAMRYGSPVIVASTGGGLVDIVTKEGVTGFHMGALNPVECDADVPDAI 567  
QY 464 AATVRRASEVFAGGRYPPEMVANCISQDLSWSKPAKWEGLEEVY-----GKG--VAT 516  
Db 568 SKTVKRALAVYGTPTAFETIILKNCMAQDLSWKPAKEWEVLLSLGVPGSPGSDGEIAP 627  
QY 517 AKKEIKVP 525  
Db 628 QAKENVATP 636  
  
RESULT 2  
US-10-138-075-2  
; Sequence 2, Application US/10138075  
; Publication No. US20030087369A1  
; GENERAL INFORMATION:  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Karlene H.  
; APPLICANT: Harvell, Leslie T.  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Orozco, Emil M.  
; TITLE OF INVENTION: Granule-Bound Starch Synthase  
; FILE REFERENCE: BB1474 NA  
; CURRENT APPLICATION NUMBER: US/10/138,075  
; PRIOR FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/288,315  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 2  
; LENGTH: 609  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-138-075-2  
  
Query Match 51.8%; Score 1433.5; DB 9; Length 609;  
Best Local Similarity 52.3%; Pred. No. 1.6e-111;  
Matches 288; Conservative 75; Mismatches 139; Indels 49; Gaps 11;  
  
QY 2 LDIWVAEAVAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRYDOYADADWTSVVVDI- 60  
Db 81 MTIVFATEVHPWCKTGGLGVDVGGVGLPPALAAAGHRVMTIAPRYDOYKDAWDTSVIVEVN 140  
QY 61 MG---EKVYFHSIKKGVRHWIDHPWFLAKVWCKTSGSKLYGPRSGADYLDNKKRFALFC 117  
Db 141 IGDIVETVRFHCYKRGVDRVFDVHPFLEKVGWKTGAKLYGPTTGTDYRNQLRFLC 200  
QY 118 KAAIEAARVLPF-----GP-GEDEVFVANDWHSALVPVLLKDYQPKGQFTKAKSVLA 169  
Db 201 LAALAPRVNLNNSEYSGYGEDVVFVANDWHTAILPCYLKSMYKNGIYKNAKAVFC 260  
QY 170 IHNIAYQGRMEEAFKDKLPQAAFDKLAFSYGAKVYTEATPMEDEKPLTGTYYKI 229  
Db 261 IHNIAYQGRFARADELLNPDSFLPSDFIDGHVK-----PVVG---RKL 303  
QY 230 NWLKGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRA-----KGIEGIVNGMOTEEWNPKT 288  
Db 261 IHNIAYQGRFARADELLNPDSFLPSDFIDGHVK-----PVVG---RKL 303  
QY 230 NWLKGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRA-----KGIEGIVNGMOTEEWNPKT 288

Db 304 NWKAGIILSDLVLTSPHYVKELTSGDPKGVDELGVLRTKPLEIGIVNGMDVEMDPST 363  
QY 289 DKFELSPYQNSYAGKAAKALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAAALPK 348  
Db 364 DKYISAKYDATTVEARALNKRLEQAEVGLPVDSSIPVIVFVGRLEEQKSGDILIAAIE 423  
QY 349 ILATPKVQIAILGTGAAYEKUNAGTKYKGRAGKGVVKSAPLAHMLTAGADPMLVPSR 408  
Db 424 FVG-ENVOIILVLTGTKKMEELTQLEVKYPNNARGIAKFNVLAHMFPAGADFIIVPSR 482  
QY 409 FEPFCGLIOLHAMHYGVPPVASTGGGLVDIVTKEGVTGFHMGALNP--DKLDEADADALAA 466  
Db 483 FEPFCGLIOLQCMRYGVPICSSITGGGLVDIVTKEGVTGFHMGSEFVCECTVDPADTAVAST 542  
QY 467 VRRASEVFAGGRYPPEMVANCISQDLSWSKPAKWEGLEEVYKVG-----GV 514  
Db 543 VTRALKQYDTPAFHEMVQNCMAQDLSWKPAKKW---EEVLLGLGVGEGSRAGIDDAEII 598  
QY 515 ATAKKEIKVP 525  
Db 599 APLAKENVATP 609  
  
RESULT 3  
US-10-138-075-5  
; Sequence 5, Application US/10138075  
; Publication No. US20030087369A1  
; GENERAL INFORMATION:  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Karlene H.  
; APPLICANT: Harvell, Leslie T.  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Orozco, Emil M.  
; TITLE OF INVENTION: Granule-Bound Starch Synthase  
; FILE REFERENCE: BB1474 NA  
; CURRENT APPLICATION NUMBER: US/10/138,075  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/288,315  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 5  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-138-075-5  
  
Query Match 49.8%; Score 1379; DB 9; Length 599;  
Best Local Similarity 50.4%; Pred. No. 5.5e-107;  
Matches 277; Conservative 78; Mismatches 147; Indels 48; Gaps 10;  
  
QY 2 LDIWVAEAVAPWSKTGGLGVDVTGGLPIELVKRHRVMTIAPRYDOYADADWTSVVVDIM 61  
Db 72 MPILFATEVHPWCKTGGLGVDVGGVGLPPALAAAGHRVMTIAPRYDOYKDTWDTNVLVEVI 131  
QY 62 ---CEKYRHSIKKGVRHWIDHPWFLAKVWCKTSGSKLYGPRSGADYLDNKKRFALFC 117  
Db 132 VGDRTETVRFHCYKRGVDRVFDVHPFLEKVGWKTGAKLYGPTTGTDYRNQLRFLC 191  
QY 118 KAAIEAARVLPF-----GP-GEDEVFVANDWHSALVPVLLKDYQPKGQFTKAKSVLA 169  
Db 192 LAALAPRVNLNNSEYSGYGVNVFVANDWHTAVLPCYLKSMYKNGIYVNAKAVFC 251  
QY 170 IHNIAYQGRMEEAFKDKLPQAAFDKLAFSYGAKVYTEATPMEDEKPLTGTYYKI 229  
Db 252 IHNIAYQGRFPRVDFELNLPESFMPSEDFVIGHVK-----PVVG---RKL 294  
QY 230 NWLKGIIAADKLIVTSPNYATEIAADAAGGVDELTVIRA-----KGIEGIVNGMOTEEWNPKT 288  
Db 295 NWKAGITECDVVLIVTSPHYVKELTSGPKGVDELGVLRKAPLETGIVNGMDVVDWNPAT 354  
QY 289 DKFLSAPYQNSYAGKAAKALQAEGLGVPDPTAPLFAFAGRLSEOKGVDIILAAALPK 348



Db 355 DKYISVKNATVAEARLNKEILQAEVGLPVDSSIPVIVFICRLEEQKSGDILIAAIP 414  
QY 349 ILATPKVQIALGTGKAAEKLVAIGIKYKRAKGVVKSAPLAHMLTAGADEMLVPSR 408  
Db 415 FL-ENVOVLIVGTGKKWEEELMLLEAKYPONARGIAKFNVLPLAHMFAGANFIIVPSR 473  
QY 409 FEPGGLIOLHAMHYGTVPVASTGGVLDVDRVKEGVTGFHMGALNP--DKLDEADADALAAT 466  
Db 474 FEPGGLIOLQGRYGVIPICSTGGVLDIVSEGVTFGHMGSNVFEFTVDPADVAASVN 533  
QY 467 VRRASEVFAAGRYPEMWANCISQDLSWSKPAQKWEGLLEEVYVYKRG-----GVA 515  
Db 534 VTRALKQYKTPSFHAMVONCAQDLWSKGPAAKW---EELGLGVESQPGIEGEETA 589  
QY 516 TAKKEEIKVP 525  
Db 590 PLAKONVATP 599

## RESULT 4

US-09-952-677-2

; Sequence 2, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; Lorz, Horst

; Lutticke, Stephanie

; Walter, Lennart

; Froberg, Claus

; Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; FROM WHEAT WHICH ARE INVOLVED IN STARCH

; SYNTHESIS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish &amp; Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,677

; FILING DATE: 14-Sep-2001

; PRIORITY INFORMATION DATA:

; APPLICATION NUMBER: 09/196,390

; FILING DATE: 19-No. US20020138876A1-1998

; APPLICATION NUMBER: DE 196 21 588.9

; FILING DATE: 29-MAY-1996

; APPLICATION NUMBER: DE 196 36 917.7

; FILING DATE: 11-SEP-1996

; APPLICATION NUMBER: PCT/EP97/02793

; FILING DATE: 28-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley, Jr., James F.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: AGREVO-9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 671 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

Query Match 31.7%; Score 878; DB 10; Length 671;  
Best Local Similarity 39.9%; Pred. No. 5.3e-65;  
Matches 210; Conservative 78; Mismatches 164; Indels 74; Gaps 16;

QY 4 IVVAAEVAPWSKTGGTGLDVTGGLPLTELVKRGRHVMTIAPRY-----DOYADAWDTSVV 57  
Db 56 IVFVTGEAAPYAKSGGLGDCVSLPTALAAARGHRVVMVPRYLNGSSDKNYAKALYTAH 115  
QY 58 VDIM-----GEKVYRHSIKKGVHRVWIDHPWFLAKWGTGKSLYGRSGADYLDNHRF 113  
Db 116 IKIPCGGSHVEVTFEYHNDVNDWVEFDDP-----SYHRPGS-LYGNFCA-PGDNQFRY 168  
QY 114 ALFCKAAIEAARVLPFGP---GEDCVFVANDHSAIVPVLLKDEYQPKQFTKAKSVLAI 170  
Db 169 TLICYAACEAPLILELGGVYIGONCMFVNDHSAIVPVLLAAKRYGYVYRDSRSTLVI 228  
QY 171 HNIATQGRMWEAEFKDKLPQAAFKLAFSDGYAKYVYTEATPMEDEKPLGKTYKKTIN 230  
Db 229 HNLAHQGVPEASTYPLGLPPEWYGALEW-----VPEWARRHALDKG-----EAVN 275  
QY 231 WLKGGILAADKLVTYSPNYATEIAADAAGVVELDVI--RAKGIEGIVNGMDIEWNPKT 288  
Db 276 FLKGAVTADRLVTVSQGSWEVTT-AEGGQGLNELLSRKSIVLNGVINGIDINDWNPPT 334  
QY 289 DKFLSAPYDQNSVYAGKAAAKEALQAEGLPVDPTAPLFAFTRGLEEQKGVDIILAALEPK 348  
Db 335 DKCLPHYSVDDL-SGKAKCAELQELGLPVREDVPLIGFIRGLDYQKGLILKMAIPE 393  
QY 349 ILATPKVQIALGTGKAAEKLVAIGIKYKRAKGVVKSAPLAHMLTAGADEMLVPSR 408  
Db 394 LM-REDVOFVMLGSGDPIFEGWMRSTESSYKDKFRGWGFSVPVSHRITAGCDILLMPER 452  
QY 409 FEPGGLIOLHAMHYGTVPVWASTGGVLDIVK-----EGVTGFHMGALNPKLDEAD 459  
Db 453 FEPGGLNQLIAMQYGTVPVWHTGTGRDVTETNFPFGAKGEETGWFSPITVDKMLWA- 511  
QY 460 ADALAAVVRASEVFAGGRYPEMVANCISQDLSWSKPAQKWEGLLE 505  
Db 512 -----LRTAMSTERE-----HKPS--WEGLMK 531

## RESULT 5

US-09-952-677-6

; Sequence 6, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; Lorz, Horst

; Lutticke, Stephanie

; Walter, Lennart

; Froberg, Claus

; Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; FROM WHEAT WHICH ARE INVOLVED IN STARCH

; SYNTHESIS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish &amp; Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/952,677

; FILING DATE: 14-Sep-2001

; PRIOR APPLICATION DATA:

RESULT 6  
US-10-163-214-6  
; Sequence 6, Application US/10163214  
; Publication No. US20030097688A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Karlene H.

```

RESULT 7
US-10-163-214-12
: Sequence 12, Application US/10163214
: Publication No. US20030097688A1
: GENERAL INFORMATION:
: APPLICANT: Allen, Stephen M.
: APPLICANT: Broglie, Karen E.
: APPLICANT: Butler, Karlene H.
: APPLICANT: Thorpe, Catherine J.
: TITLE OF INVENTION: Starch Synthase Isoform V
: FILE REFERENCE: BB1520 US NA
: CURRENT APPLICATION NUMBER: US/10/163,214
: CURRENT FILING DATE: 2002-06-05

```

;; PRIOR APPLICATION NUMBER: 60/297,099  
;; PRIOR FILING DATE: 2001-06-08  
;; NUMBER OF SEQ ID NOS: 13  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 12  
;; LENGTH: 914  
;; TYPE: PRT  
;; ORGANISM: Triticum aestivum  
US-10-163-214-12

Query Match 19.8%; Score 549; DB 9; Length 914;  
Best Local Similarity 30.8%; Pred. No. 2.7e-37;  
Matches 169; Conservative 89; Mismatches 202; Indels 88; Gaps 22;  
QY 2 LDIVVAAEAPWPSKTGGGLDVTGGLPIELVKGHRVMTIAPRYD-QYADAWDTSVVVDI 60  
DB LHIAHIAEMAPVAVKVGGLADVISGLKALOKKGLHVEILPKYDCMQHNOINNLKVLVD 480  
QY 61 MGEKRYFHSIKKGVRHWIDHPWFLAKVWGKT--GSKLY--GPR-----SGADYLDNH 110  
DB LVQS--YF-----EGNPNKIKWTGTEVGLPVFIETPOHPAMFTSRAQYGEH 526  
QY 111 ---KRALPCKAAIEAARVLPFGEDC-VFVANDWHSALVPVLLKDEYQPKGQFTKAKS 166  
DB 527 DDFKRFYSFSAALE---LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI 581  
QY 167 VLATHNIAFOGRMWEAEAFKDTKLPOAADFCLAFSDGYAKVYTEATPMEDEKPP-LTGT 225  
DB 582 CFTCHNEFYQG-----TAPARDLAWC-----GLDVEHLDRPDRMDS 619  
QY 226 YKINLWKGIIAADKLVTSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWN 285  
DB 620 HGRINAVKAVYSNIVTVPYALEVRSESGRGLQDTLKVHKKFVGLINGIDTDTWN 679  
QY 286 PKDKFLSAPYQNSVYAGKAAKEALQAEGL-PVDPTAPLFAFIRLEQKGVYDIIIA 344  
DB 680 PCDRYLKQVYNADL-QCKAANKAALREQLNLASVPSQPLVGCITFLVAQKGVHLIRH 738  
QY 345 ALPKILATPKVOJAILGTGKAAEKLVAIGTKYKGR-----VPEIQREFEGADHFNQNNIRLILKYDALSHC 791  
DB 739 AIYK-TAELGGQFVLLGSSP-----VPEIQREFEGADHFNQNNIRLILKYDALSHC 791  
QY 396 LTAGDFMLPSRPEPCGLIQLHAMHYGTVPVASTGGGLVDTV---KEGVTGTFHMGALN 451  
DB 792 IYAASDMFVPSIPEPCGLITQMIAMRYGSPVIVKTKGLNDSVDFDDEITP---MEVRN 848  
QY 452 PDKLDEADALATVRRASEVFAGGRYPPEMVANCISQDL-----SWSKPAQKWEGLLEE 507  
DB 849 GFTFVKADEQGLSAMESAFNCYT--RKPEVWKOLVOKDMTIDFSWDTISASQYEDIYOKA 906  
QY 508 VYKGGVA 515  
DB 907 VARARAVA 914

RESULT 8  
US-10-163-214-2  
; Sequence 2, Application US/10163214  
; Publication No. US20030097688A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Katherine H.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Starch Synthase Isoform V  
; FILE REFERENCE: BBI520 US NA  
; CURRENT APPLICATION NUMBER: US/10/163,214  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/297,099  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 2

;; LENGTH: 909  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
US-10-163-214-2

Query Match 19.7%; Score 545; DB 9; Length 909;  
Best Local Similarity 29.4%; Pred. No. 5.8e-37;  
Matches 159; Conservative 92; Mismatches 199; Indels 90; Gaps 20;

QY 2 LDIVVAAEAPWPSKTGGGLDVTGGLPIELVKGHRVMTIAPRYD-QYADAWDTSVVVDI 60  
DB LHIVHIAEMAPVAVKVGGLADVISGLKALOKKGLHVEILPKYDCMQHNOINNLKVLVD 475  
QY 61 MGEKRYFHSIKKGVRHWIDHPWFLAKVWGKT--GSKLY--GPRSGADYL-----107  
DB 476 -----VVKSYFEGNMFANKIWTGTEVGLPVFIETPOHPGFFWRAQYGEH 521  
QY 108 DNHRKRALPCKAAIEAARVLPFGEDC-VFVANDWHSALVPVLLKDEYQPKGQFTKAKS 166  
DB 522 DDFKRFYSFSALE---LLYQSGKKVDIIHCHDWQTAFAVAPLYWDVYANLG-FNSARI 576  
QY 167 VLATHNIAFOGRMWEAEAFKDTKLPOAADFCLAFSDGYAKVYTEATPMEDEKPP-LTGT 226  
DB 577 CFTCHNEFYQG-----IAPQDLAYCGLDVBDRPDR--MRDNSH 615  
QY 227 KINLWKGIIAADKLVTSPNYATEIAADAAGGVELDTVIRAKGIEGIVNGMDIEWN 286  
DB 616 GRINAVKAVYSNIVTVPYALEVRSESGRGLQDTLKVHKKFVGLINGIDTDTWN 675  
QY 287 KDKFLSAPYQNSVYAGKAAKEALQAEGL-PVDPTAPLFAFIRLEQKGVYDIIIA 345  
DB 676 STDRELFKQVYSANDLY-GKSANKAALRKQLKASTOASQPLVGCITRLVPQKGVHLIRH 734  
QY 346 LPKILATPKVOJAILGTGKAAEKLVAIGTKYK--GRAGKGVVFSAPLAHMLTAGADF 402  
DB 735 YKITELEG-QFVLGSSPQVHQIREFEGADHFNQNNIRLILKYDALSCH 793  
QY 403 MLVPSRPEPCGLIQLHAMHYGTVPVASTGGGLVDTV---KEGVTGTFHMGAL 450  
DB 794 FIVPSMEPCGLTQVMAMRYGSPVIVKTKGLNDSVDFDDEITPMEVRNGTTEL-----848  
QY 451 NPDKLDEADALATVRRASEVFAGGRYPPEMVANCISQDL-----SWSKPAQKWEGLLEE 506  
DB 849 ---KADEQD---FGNALERAFNY--HRKPEVWKOLVOKDMKIDFSWDTISASQYEDIYOK 900

RESULT 9  
US-10-163-214-13  
; Sequence 13, Application US/10163214  
; Publication No. US20030097688A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Katherine H.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Starch Synthase Isoform V  
; FILE REFERENCE: BBI520 US NA  
; CURRENT APPLICATION NUMBER: US/10/163,214  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/297,099  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 13  
; LENGTH: 874  
; TYPE: PRT  
; ORGANISM: Vigna unguiculata  
US-10-163-214-13

Query Match 19.4%; Score 537; DB 9; Length 874;  
Best Local Similarity 30.4%; Pred. No. 2.6e-36;  
Matches 166; Conservative 85; Mismatches 191; Indels 108; Gaps 25;

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QY 2 LDIVMAAEVAPWSKTGGLDVGTGGLPIELVKRGHRVMTIAPRYD--QYADAMDTSVVVD 59
Db 377 LYVIHTAAEMAPVAKVGGGLGDLVLSGLSKALQKKGHLVEIILPKYDCMQYDRIGDLR-ALD 435
QY 60 IMGEKVRYPHSIKKGVHRVWIDHPWFLAKVWGKT--GSKLY-----GPRSGA 104
Db 436 VVIES--YF-----DGOLEFKNKIWGTVEGLPVYIFEPHHPGKFFWRGDIYGA 481
QY 105 DYLDNHRKRALFCKAALAEARVLPGFGEDCVFVANDWHSALVPVLLKDEYQKGFQTKA 164
Db 482 H--DDFRFYSYFRAALEF--LLQAGKKPDIH-CHDWQTAFTAPLWYDYAPKG-LNSA 535
QY 165 KSVLAHNTAFQGRMWEAFKDTKLPQAAFDKLAFLSDGYAKVYTEATPMEDEKPLTGK 224
Db 536 RICTCHNPFYQCTAGASELFCGLDQSHQNLN-----PDRMQDN-----S 575
QY 225 TYKKNLWKGIIIAADKLVTSPNYATEIAADAGGVDELDTVI--RAKGIEGVNGMDIE 282
Db 576 AHNRVNSVGAVVYSNITVTSPYAOEVRT-AEGGKGLHSTLSTHSKKEIGILGIDTD 634
QY 283 EWNPKTDKFLSAPYDQNSVYAGAAKAEALQAEGLL-PVDPPTAPLFAFICRLEBQKGVDI 341
Db 635 IWPATDPFFLOVQYNANDL--QKSENKEALRNGLSSADVRRPLVCCITRLVPQKGVHL 693
QY 342 ILAALPKILATPKV--QIAILGTCKAAAYEKLVAIGTKYKGRA-----KGWKFSA 390
Db 694 IRHA---LYLTLEGGQFVLLGSSPVPH-----IQREFEIGIANHFQNHDIRLILKYDE 744
QY 391 PLAHMLTAGADFMVLPSRPFPCGLIQLHAMHYGVVAVSTGGGLVDIV-----438
Db 745 SLSHAIYAASDMFLIPISFEPFPGGLTOMISRYGAIPARTGGGLNDSFVDDDTIPSQF 804
QY 439 KEGVTGFHMGALNPKLDEADALAAATVRRASEVFAAG--RYPEMVANCISQDLNSKP 496
Db 805 RNGET-----FLNAD--EKGINDALV-----RAINLFTNDPKSWKQLVKQKMNIDFSWDSS 853
QY 497 AQKWEGLEEVV 508
Db 854 AAQVEELYSKSV 865

RESULT 10
US-10-007-693-99
; Sequence 99, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 99
; LENGTH: 474
; TYPE: PRK
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-99

Query Match 14.8%; Score 410.5; DB 12; Length 474;
Best Local Similarity 28.2%; Pred. No. 4.le.26;
Matches 148; Conservative 72; Mismatches 206; Indels 99; Gaps 22;

QY 2 LDIVMAAEVAPWSKTGGLDVGTGGLPIELVKRGHRVMTIAPRYDQYADAMDTSVVVDIM 61
Db 1 MKLIHTALEFAPVIAKAGGLGALYGL-AKALAANTTEVPIPLFKLTLPEQDLCSI- 58
QY 62 GEKVRYF-----HSIKKGVHRVWIDHPWFLAKVWGKTGSKLYGPRSGADYL 107
Db 59 -QKLSYFFPAGEQEAATAFSVYEGIKVTLFKL-----DTQPELFENAEITLYTS 104
QY 108 DNHKRALFCKAAI-----EAARVLPFGGEDCVFVANDWHSALVPVLLKDEYQKGFQ 162

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Db 105 DDARFCFAFAAASYYIQEGANIVHL-----HDWHTGLVAGLLKQ--QPCSQLQ 152
QY 163 KAKSVLAHNTAFQGRMWEAFKDTKLPQAAFDKLAFLSDGYAKVYTEATPMEDEKPLT 222
Db 153 KI-VLTLHNFGRGYTTRILEASSLNE-----FYISOYQLFRDPQTCVL 196
QY 223 GKYTKKNLWKGIIIAADKLVTSPNYATEIAADAGGVDELDTVIRAK--GIEGIVNGMD 280
Db 197 -----LKGALYCSQDFVTTSPTYAKELLEDYS-DYELHDAITARQHHLRGILNGID 246
QY 281 IEWNPKTDFLSAPYDQ-----NSVYAGAAKAEALQAEGLPVPDPTAPLFAFICRLE 334
Db 247 TTIMGPTEDNPLAKNYTKELFETPSIFFEAKAENKKALYERLGLSLE-HSPCVILISRIA 305
QY 335 EOKGVDIILALPKILATPKVQIAILGT--CKAAAYEKLNV--AIGTKYKGRAGVWKFES 389
Db 306 EOKGPHFMKOAIIHALENAYTLI-IIGTCYGNQLHEEFANLQESIANSPDVRI--LLTYS 362
QY 390 APLAHMLTAGADFMVLPSRPFPCGLIQLHAMHYGVVAVSTGGGLVDTVKGVTFGHMGA 449
Db 363 DVLARQIFAAADMICIPSMFEPFGLTOMIGMRYGTPLVRATGGGLADTVANGINGFSF-- 420
QY 450 LNP-DKLDEADADALAAATVRRASEVFAAGRYPEMVANCI--SQDL 491
Db 421 FNPHDFEFRNMLSEAVITYTNNH-----DKWQHIVRACLDFSSDL 461

RESULT 11
US-10-007-693-69
; Sequence 69, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007,693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 69
; LENGTH: 476
; TYPE: PRK
; ORGANISM: Chlamydia pneumoniae
US-10-007-693-69

Query Match 14.5%; Score 402.5; DB 12; Length 476;
Best Local Similarity 26.9%; Pred. No. 1.9e-25;
Matches 150; Conservative 78; Mismatches 204; Indels 125; Gaps 24;

QY 4 IVMVAEAVAPWSKTGGLDVGTGGLPIELVKRGHRVMTIAPRY--DOYADAMDTSVVVDI 60
Db 3 IVQVAVEETPIVKVGGGLGDAVASLSKELAKQ-NDVEVLLPHYPLISKFSS-----QV 54
QY 61 MGEKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTGSKLYGP-----RSGAD 105
Db 55 LRSERSFYB-----FLGQQAASALSYSEGLLTLITLDSQIELSTISV 99
QY 106 YLDNHRKRALFCKAALAEARVLPGFGEDCVFVANDWHSALVPVLLKDEYQKGFQTKA 164
Db 100 YSENNVVRSAFAAAA--AAYLQEAADPAD--IVHLHDWHVGLLAGLLKNLNP-----VHS 151
QY 165 KSVLAHNTAFQGRMWEAFKDTKLPQAAFDKLAFLSDGYAKVYTEATPMEDEKPLTGK 224
Db 152 KIVFTIHNFGYRG-----YCSTQLLAAS---QIDDFHLSHY-----QLFRDPQTSV 194
QY 225 TYKKNLWKGIIIAADKLVTSPNYATEIAADAGGVDELDTVIRAK--IEGIVNGMDIE 282
Db 195 L-----MGALYCSDYITVTSLTYQELIINDYS-DYELHDALLARNSVFSGLINGIDED 247
QY 283 EWNPKTDKFLSAPYD-----QNSVYAGAAKAEALQAEGLPVPDPTAPLFAFICRLEEQ 336

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Db 248 VNNPKTDPALAVQYDASLLSEPOVLFTKKEENRAVLYEKLGISSD-YFPLICVISRIVEE 306  
QY 337 KG-----VDLILALPKILATPKVQVAILGTGKAAAEKLVNAIGTKYKGRAG-----VVK 387  
Db 307 KGPFWKEIILHAMSHSYA-----FILIGTSQ--NEVLNFEFNLDQCLASSPNIRLILD 359  
QY 388 FSAPLAHMLTAGADEMLVPSRPEPCGLIOLHAMHYGTVPVASTGGLVTVKEGVTGFM 447  
Db 360 FNDPLARLYAADMICIPSHREACGLIOLIAMRYGTVPVIRKGTGLADTVIPGVNGFTF 419  
QY 448 GALNPKDLDEADALAAATVRRASEVFAGGRYPYEMVANCISODLSWSPAKQWGLLEEV 507  
Db 420 --FDTNNE-----FRAMLSNAVT---YRQEPDWLNLIESG 453  
QY 508 VYKGVGVATKEELKV 524  
Db 454 MLRASGLDAMAKHYVNL 470  
RESULT 12  
US-10-163-214-10  
; Sequence 10, Application US/10163214  
; Publication No. US20030097688A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: Butler, Karen H.  
; APPLICANT: Thorpe, Catherine J.  
; TITLE OF INVENTION: Starch Synthese Isoform V  
; FILE REFERENCE: BRL520 US NA  
; CURRENT APPLICATION NUMBER: US/10/163,214  
; PRIOR FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/297,099  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 10  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-163-214-10

Query Match 13.9%; Score 385.5; DB 9; Length 293;  
Best Local Similarity 33.0%; Pred. No. 2.5e-24;  
Matches 101; Conservative 59; Mismatches 115; Indels 31; Gaps 9;  
QY 228 KINWLKGGIITADKLVTVSPNYATEIAADAGGVDELDTVIRAKGIEGIVNGMDIEWNPK 287  
Db 1 KINAVGAVVYSNITVTTSPTALVLRSEGGRLQDTLKVHSRFLGILNGIDTWNPC 60  
QY 288 TDRFLSAPYDQNSVYAGKAAKALQALGLI-PVDPTAPLEAFTRLEEQKGVDTIILAL 346  
Db 61 TDRLYKVOYNAKL-QGKAANKALRQLNLASAYSOPVLGCLTRILVAQKGVHLIRHAI 119  
QY 347 PKILATPKVQVAILGTGKAAAEKLVNAIGTKYKGRA-----KGWVKSAPLAHMLT 397  
Db 120 YK-TAELGGQVLLGSSP-----VPEIQREFEGIAHFQNNNIRILIKYDDALSICII 172  
QY 398 AGADEMLVPSRPEPCGLIOLHAMHYGTVPVASTGGLVDTV-----KEGVTGFHMGALNPD 453  
Db 173 AASDMFTVPSIFPCGGLTQMIAMRYGVPVIRKGTGLNDSVDFDDTIP---MEVNGF 229  
QY 454 KLDEADALAAATVRRASEVFAGGRYPYEMVANCISQDL-----SWSKPAQKWGLLEEVY 509  
Db 230 TFWKDEQGLSSAMERAFNCYT--RKPEVKNQVLQVKDMTIDFSWDTASQYEDIYQAVA 287  
QY 510 KGKGA 515  
Db 288 RARAVA 293

RESULT 13  
US-09-739-438-2

; Sequence 2, Application US/09739438  
; Patent No. US20020029394A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Beckles, Diane M.  
; APPLICANT: Thorpe, Cathy  
; TITLE OF INVENTION: Homologs of Starch Synthese D01  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/739,438  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: 60/171514  
; PRIOR FILING DATE: 1999-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 2  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-739-438-2

Query Match 7.8%; Score 215.5; DB 10; Length 117;  
Best Local Similarity 46.6%; Pred. No. 1.1e-10;  
Matches 41; Conservative 17; Mismatches 25; Indels 5; Gaps 1;  
QY 356 QIAILGTG-----KAAEKLVAIGTKYKGRAGVGVKFSAPLAHMLTAGADEMLVPSRFE 410  
Db 8 QVVLGSGAPDHRIOGDETNIASKLHGEGYHGVKLCITYDEPLSHLIYAGADFILVPSMFE 67  
QY 411 PCGLIOLHAMHYGTVPVASTGGLVDTV 438  
Db 68 PCGLTQLTAMRYGSIPIVRKTKGLYDTV 95

RESULT 14  
US-09-738-626-4738  
; Sequence 4738, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 4738  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4738

Query Match 7.4%; Score 206; DB 9; Length 409;  
Best Local Similarity 27.2%; Pred. No. 4.2e-09;  
Matches 83; Conservative 47; Mismatches 127; Indels 48; Gaps 15;  
QY 210 ATPWEDE--KPPLTGTYKKINML-KGGIADKLVTVSPNYATEIAADAGGVDELDTV 266  
Db 129 AHSLEPDRPWKRGQGGYDVSSWSEKNAMEYADAVTAVSARMKDSILA-AYPIEPDNV 187

